

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:06 ; Search time 43.3077 Seconds
(without alignments)
71.766 Million cell updates/sec

Title: US-09-787-443A-9

Perfect score: 11

Sequence: 1 ATNKKTGRRPR 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 22883

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : A_Geneseq_29Jan04:
1: geneseqp1980s:
2: geneseqp1990s:
3: geneseqp2000s:
4: geneseqp2001s:
5: geneseqp2002s:
6: geneseqp2003as:
7: geneseqp2003bs:
8: geneseqp2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	11	100.0	11	3	AAY88537	Aay88537 NCAM Ig1
2	11	100.0	11	5	ABG69337	Abg69337 Human neu
3	4	36.4	11	2	AAR40873	Aar40873 SSP for f
4	4	36.4	11	2	AAY20756	Aay20756 Human neu
5	4	36.4	11	2	AAY39668	Aay39668 Tat-inhib
6	4	36.4	11	2	AAY25088	Aay25088 Transduct
7	4	36.4	11	2	AAY25086	Aay25086 Transduct
8	4	36.4	11	3	AAB26886	Aab26886 PR-39 der
9	4	36.4	11	3	AAY93554	Aay93554 Amino aci

10	4	36.4	11	3	AAY93552	Aay93552 Amino aci
11	4	36.4	11	3	AAB29435	Aab29435 Synthetic
12	4	36.4	11	3	AAB29438	Aab29438 Synthetic
13	4	36.4	11	4	AAM97944	Aam97944 Human pep
14	4	36.4	11	4	AAE04943	Aae04943 Nuclear D
15	4	36.4	11	4	AAB97278	Aab97278 PR-39 der
16	4	36.4	11	4	AAB84692	Aab84692 Amino aci
17	4	36.4	11	5	ABB82469	Abb82469 Peptide f
18	4	36.4	11	5	ABP54091	Abp54091 Transport
19	4	36.4	11	6	ABO14954	Abol4954 Microsoma
20	4	36.4	11	6	ABP60206	Abp60206 Synthetic
21	4	36.4	11	6	ABP56088	Abp56088 Protein t
22	4	36.4	11	6	ABG33050	Abg33050 Pig arg/p
23	4	36.4	11	6	ABU63113	Abu63113 Microsoma
24	4	36.4	11	7	ADB87318	Adb87318 Human pep
25	4	36.4	11	7	ADC19836	Adc19836 Fluoresce
26	4	36.4	11	7	ADC03321	Adc03321 Synthetic
27	3	27.3	11	1	AAP40439	Aap40439 Sequence
28	3	27.3	11	1	AAP50159	Aap50159 Human int
29	3	27.3	11	1	AAP82336	Aap82336 Compound
30	3	27.3	11	1	AAP82811	Aap82811 Peptide f
31	3	27.3	11	1	AAP90842	Aap90842 New brady
32	3	27.3	11	1	AAP90643	Aap90643 Signal pe
33	3	27.3	11	2	AAR09490	Aar09490 Bradykini
34	3	27.3	11	2	AAR09489	Aar09489 Bradykini
35	3	27.3	11	2	AAR09485	Aar09485 Bradykini
36	3	27.3	11	2	AAR09463	Aar09463 Bradykini
37	3	27.3	11	2	AAR09488	Aar09488 Bradykini
38	3	27.3	11	2	AAR09491	Aar09491 Bradykini
39	3	27.3	11	2	AAR09486	Aar09486 Bradykini
40	3	27.3	11	2	AAR09461	Aar09461 Bradykini
41	3	27.3	11	2	AAR09464	Aar09464 Bradykini
42	3	27.3	11	2	AAR03387	Aar03387 Fragment
43	3	27.3	11	2	AAR05912	Aar05912 Partial s
44	3	27.3	11	2	AAR08092	Aar08092 Antifreez
45	3	27.3	11	2	AAR28593	Aar28593 Partial s
46	3	27.3	11	2	AAR25458	Aar25458 wohl-5. 3
47	3	27.3	11	2	AAR26211	Aar26211 Sequence
48	3	27.3	11	2	AAR37243	Aar37243 IL-6 anta
49	3	27.3	11	2	AAR44847	Aar44847 Lactoferr
50	3	27.3	11	2	AAR38680	Aar38680 Bradykini
51	3	27.3	11	2	AAR33285	Aar33285 pDS56/RBS
52	3	27.3	11	2	AAR40874	Aar40874 SSP for f
53	3	27.3	11	2	AAR40872	Aar40872 SSP for f
54	3	27.3	11	2	AAR41634	Aar41634 SSP for f
55	3	27.3	11	2	AAR40878	Aar40878 SSP for f
56	3	27.3	11	2	AAR40870	Aar40870 SSP for f
57	3	27.3	11	2	AAR40871	Aar40871 SSP for f
58	3	27.3	11	2	AAR41635	Aar41635 SSP for f
59	3	27.3	11	2	AAR40875	Aar40875 SSP for f
60	3	27.3	11	2	AAR31485	Aar31485 P3 OF 31-
61	3	27.3	11	2	AAR54747	Aar54747 Ad5 fibre
62	3	27.3	11	2	AAR54725	Aar54725 ScFv-Ad5
63	3	27.3	11	2	AAR55163	Aar55163 Fragment
64	3	27.3	11	2	AAR67084	Aar67084 Sweet pep
65	3	27.3	11	2	AAR45679	Aar45679 Fibronect
66	3	27.3	11	2	AAR62627	Aar62627 Epidermal

67	3	27.3	11	2	AAR46491	Aar46491 Growth co
68	3	27.3	11	2	AAR71762	Aar71762 Neurotens
69	3	27.3	11	2	AAR71761	Aar71761 Neurotens
70	3	27.3	11	2	AAR71764	Aar71764 Neurotens
71	3	27.3	11	2	AAR71763	Aar71763 Neurotens
72	3	27.3	11	2	AAR54763	Aar54763 Plasminog
73	3	27.3	11	2	AAR46502	Aar46502 Growth co
74	3	27.3	11	2	AAR70293	Aar70293 Subpeptid
75	3	27.3	11	2	AAR70594	Aar70594 HIV(B35)-
76	3	27.3	11	2	AAR61397	Aar61397 PF4-relat
77	3	27.3	11	2	AAW21352	Aaw21352 Gastrin p
78	3	27.3	11	2	AAW21338	Aaw21338 Glucagon
79	3	27.3	11	2	AAR79718	Aar79718 Optimal p
80	3	27.3	11	2	AAR80937	Aar80937 MAGE-2 pe
81	3	27.3	11	2	AAR80912	Aar80912 MAGE-2 pe
82	3	27.3	11	2	AAR80062	Aar80062 Peptide u
83	3	27.3	11	2	AAR90612	Aar90612 Lactoferr
84	3	27.3	11	2	AAR87615	Aar87615 Lactoferr
85	3	27.3	11	2	AAR95097	Aar95097 Natural f
86	3	27.3	11	2	AAR91858	Aar91858 Lactoferr
87	3	27.3	11	2	AAW04653	Aaw04653 Dimeric b
88	3	27.3	11	2	AAR95265	Aar95265 nisA-(fs)
89	3	27.3	11	2	AAR96142	Aar96142 Fluorogen
90	3	27.3	11	2	AAR96435	Aar96435 Hepatitis
91	3	27.3	11	2	AAR96427	Aar96427 Hepatitis
92	3	27.3	11	2	AAR96429	Aar96429 Hepatitis
93	3	27.3	11	2	AAR96432	Aar96432 Hepatitis
94	3	27.3	11	2	AAR96436	Aar96436 Hepatitis
95	3	27.3	11	2	AAR96426	Aar96426 Hepatitis
96	3	27.3	11	2	AAR96431	Aar96431 Hepatitis
97	3	27.3	11	2	AAW10520	Aaw10520 Lactoferr
98	3	27.3	11	2	AAW10518	Aaw10518 Lactoferr
99	3	27.3	11	2	AAW17451	Aaw17451 Consensus
100	3	27.3	11	2	AAR85318	Aar85318 Human ret

ALIGNMENTS

RESULT 1
 AAY88537
 ID AAY88537 standard; peptide; 11 AA.
 XX
 AC AAY88537;
 XX
 DT 07-AUG-2000 (first entry)
 XX
 DE NCAM Ig1 binding peptide #9.
 XX
 KW NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1;
 KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;
 KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
 KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
 KW treatment; prosthetic nerve guide; treatment; nervous system.
 XX
 OS Synthetic.
 XX

PN WO200018801-A2.
XX
PD 06-APR-2000.
XX
PF 23-SEP-1999; 99WO-DK000500.
XX
PR 29-SEP-1998; 98DK-00001232.
PR 29-APR-1999; 99DK-00000592.

XX
PA (RONN/) RONN L C B.
PA (BOCK/) BOCK E.
PA (HOLM/) HOLM A.
PA (OLSE/) OLSEN M.
PA (OSTE/) OSTERGAARD S.
PA (JENS/) JENSEN P H.
PA (POUL/) POULSEN F M.
PA (SORO/) SOROKA V.
PA (RALE/) RALETS I.
PA (BERE/) BEREZIN V.

XX
PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
PI Poulsen FM, Soroka V, Ralets I, Berezin V;

XX
DR WPI; 2000-293111/25.

XX
PT Compositions that bind neural cell adhesion molecules useful for treating
PT disorders of the nervous system and muscles e.g. Alzheimer's and
PT Parkinson's diseases.

XX
PS Example 4; Page 25; 119pp; English.

XX
CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
CC NCAM is found in three forms, two of which are transmembrane forms, while
CC the third is attached via a lipid anchor to the cell membrane. All three
CC NCAM forms have an extracellular structure consisting five immunoglobulin
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
CC terminal. The present sequence represents a peptide which binds to the
CC NCAM Ig1 domain. The peptide can be used in a compound which binds to
CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite
CC outgrowth from NCAM presenting cells, and is also capable of promoting
CC the proliferation of NCAM presenting cells. The compound may be used in
CC the treatment of normal, degenerated or damaged NCAM presenting cells.
CC The compound may in particular be used to treat diseases of the central
CC and peripheral nervous systems such as post operative nerve damage,
CC traumatic nerve damage, impaired myelination of nerve fibres, conditions
CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
CC dementias, sclerosis, nerve degeneration associated with diabetes
CC mellitus, disorders affecting the circadian clock or neuro-muscular
CC transmission and schizophrenia. Conditions affecting the muscles may also
CC be treated with the compound, such as conditions associated with impaired
CC function of neuromuscular connections (e.g. genetic or traumatic shock or
CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
CC liver and bowel may also be treated using the compound. The compound is
CC used in a prosthetic nerve guide, and also to stimulate the ability to
CC learn, and to stimulate the memory of a subject

XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATNKKTGRRPR 11
| | | | | | | | | | | |
Db 1 ATNKKTGRRPR 11

RESULT 2

ABG69337

ID ABG69337 standard; peptide; 11 AA.

XX

AC ABG69337;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human neural cell adhesion molecule (NCAM) peptide #9.

XX

KW Human; neural cell adhesion molecule; NCAM; heart muscle cell survival;
KW acute myocardial infarction; central nervous system disorder; stroke;
KW peripheral nervous system disorder; postoperative nerve damage;
KW traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;
KW postischaemic damage; multiinfarct dementia; multiple sclerosis;
KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;
KW Alzheimer's disease; Parkinson's disease;
KW Huntington's disease. atrophic muscle disorder; gonad degeneration;
KW nephrosis.

XX

OS Homo sapiens.

XX

PN WO200247719-A2.

XX

PD 20-JUN-2002.

XX

PF 12-DEC-2001; 2001WO-DK000822.

XX

PR 12-DEC-2000; 2000DK-00001863.

XX

PA (ENKA-) ENKAM PHARM AS.

XX

PI Bock E, Berezin V, Kohler LB;

XX

DR WPI; 2002-583473/62.

XX

PT Use of a compound comprising a peptide of neural cell adhesion molecule,
PT in the preparation of medicament for preventing death of cells presenting
PT NCAM or NCAM ligand and treating central nervous system diseases.

XX

PS Disclosure; Page 15; 57pp; English.

XX

CC The invention relates to use of a compound (I) comprising a peptide which
CC comprises at least 5 contiguous amino acid residues of a sequence of the
CC neural cell adhesion molecule (NCAM), its fragment, variant or its mimic,
CC for the preparation of a medicament for preventing death of cells

CC presenting the NCAM or an NCAM ligand. (I) is useful in the preparation
CC of a medicament for preventing death of cells presenting the NCAM or an
CC NCAM ligand. The medicament is for the stimulation of the survival of
CC heart muscle cells, such as survival after acute myocardial infarction.
CC The medicament is for the treatment of diseases or conditions of the
CC central and peripheral nervous system, such as postoperative nerve
CC damage, traumatic nerve damage, e.g. resulting from spinal cord injury,
CC impaired myelination of nerve fibres, postischaemic damage, e.g.
CC resulting from a stroke, multiinfarct dementia, multiple sclerosis, nerve
CC degeneration associated with diabetes mellitus, neuro-muscular
CC degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease and
CC Huntington's disease. The medicament is for the treatment of diseases or
CC conditions of the muscles including conditions with impaired function of
CC neuro-muscular connections, such as genetic or traumatic atrophic muscle
CC disorders, and for the treatment of diseases of conditions of various
CC organs, such as degenerative conditions of the gonads, pancreas (e.g.
CC diabetes mellitus type I and II) and kidney (e.g. nephrosis). ABG69329-
CC ABG69352 represent human NCAM peptides of the invention

XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATNKKTGRRPR 11
|||||||||||
Db 1 ATNKKTGRRPR 11

RESULT 3

AAR40873

ID AAR40873 standard; protein; 11 AA.

XX

AC AAR40873;

XX

DT 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 28-MAR-1994 (first entry)

XX

DE SSP for flavonoid-3',5'-hydroxylase gene product.

XX

KW Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;

KW tobacco; pigment alteration; blue; SSP; single specific primer; PCR;

KW polymerase chain reaction; amplification; expression.

XX

OS Petunia x hybrida.

XX

PN WO9318155-A1.

XX

PD 16-SEP-1993.

XX

PF 20-NOV-1992; 92WO-JP001520.

XX

PR 02-MAR-1992; 92JP-00044963.

XX

PA (KYOW) KYOWA HAKKO KOGYO CO LTD.

XX
PI Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;
PI Okinaka Y;
XX
DR WPI; 1993-303469/38.
DR N-PSDB; AAQ47874.
XX
PT Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to
PT transform plants e.g. petunia, rose or tobacco to give bluer flower
PT colour and altered pigment pattern.
XX
PS Claim 11; Page 56; 82pp; Japanese.
XX
CC Insertion of the sequences (AAQ47840-42) into plants such as rose,
CC petunia, tobacco and carnation, using a suitable vector such as
CC agrobacterium, give transformed plants which express the gene, resulting
CC in petals with a bluer colour than normal, and/or pigmentation patterns
CC which do not occur naturally. The sequences were amplified using primers
CC (AAQ47843-70). Related single specific primers using a gene sequence
CC coding for the haem-binding region of cytochrome P450 are shown in
CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 TGRR 9
Db 4 TGRR 7

RESULT 4
AAY20756
ID AAY20756 standard; protein; 11 AA.
XX
AC AAY20756;
XX
DT 22-JUL-1999 (first entry)
XX
DE Human neurofilament-M mutant protein fragment 38.
XX
KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW frameshift mutation; age-related disease; neurodegenerative disorder;
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
KW high mobility group protein-C; neuroendocrine specific protein A.
XX
OS Synthetic.
OS Homo sapiens.

XX
PN WO9845322-A2.
XX
PD 15-OCT-1998.
XX
PF 02-APR-1998; 98WO-IB000705.
XX
PR 10-APR-1997; 97US-0043163P.
XX
PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
PA (UYRO-) UNIV ROTTERDAM ERASMUS.
PA (UYUT-) RIJKSUNIV UTRECHT.
XX
PI Van Leeuwen FW, Grosveld FG, Burbach JPH;
XX
DR WPI; 1998-609901/51.
DR N-PSDB; AAX75759.
XX
PT Diagnosing disease by detecting frameshift mutations in RNA or
PT corresponding protein mutations - used to diagnose cancer and
PT neurological diseases, particularly Alzheimer's disease, and also for
PT treatment and prevention with specific ribozymes or wild-type RNA.
XX
PS Disclosure; Fig 8; 258pp; English.
XX
CC This invention describes a novel method for the diagnosis of a disease
CC caused by, or associated with, an RNA molecule that has a frameshift
CC mutation. The method is used to diagnose age-related diseases, especially
CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
CC and many others listed) or susceptibility to these disorders. The method
CC allows a definitive diagnosis of Alzheimer's disease in living patients,
CC at an early stage. It is based on the observation that disease may be
CC caused by mutations in RNA rather than DNA. The invention describes the
CC used of neuronal system RNA molecules, specifically proteins including
CC beta-amyloid precursor protein (beta-APP), the microtubule associated
CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
CC protein-C (HMGP-C) and neuroendocrine specific protein A
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATNK 4
|||
Db 4 ATNK 7

RESULT 5
AAY39668

ID AAY39668 standard; peptide; 11 AA.
XX
AC AAY39668;
XX
DT 24-NOV-1999 (first entry)
XX
DE Tat-inhibitory peptide.
XX
KW TAT-inhibitory peptide; HIV; therapy; viral infection; AIDS.
XX
OS Synthetic.
XX

FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "acetylated"
FT Misc-difference 10
FT /note= "D-form residue"
FT Modified-site 11
FT /note= "(biotin)-Cys-NH2"
XX

PN WO9947173-A2.

XX
PD 23-SEP-1999.

XX
PF 19-MAR-1999; 99WO-US005914.

XX
PR 19-MAR-1998; 98US-00044411.

XX
PA (UYNE-) UNIV NEW JERSEY.

XX
PI Stein S, Leibowitz MJ;

XX
DR WPI; 1999-561868/47.

XX
PT New carriers for in vivo delivery of therapeutic agent, comprising a
PT polymer having a conjugated thiol compound which can form a disulphide
PT group with a thiol group of the agent.

XX
PS Claim 19; Page 54; 74pp; English.

XX
CC This sequence represents a Tat-inhibitory peptide, that can be used in
CC the carrier of the invention. The carrier is for in vivo delivery of a
CC therapeutic agent, and comprises a thiol group comprising a polymer, and
CC at least one thiol compound conjugated to the polymer such that the thiol
CC group of the thiol compound and the thiol group of the therapeutic agent
CC can form a disulphide bond. The carriers can be used for the delivery of
CC therapeutic agents such as HIV Tat-inhibiting polypeptides for the
CC treatment of viral infections such as AIDS. The carrier does not
CC interfere with the bioavailability of the therapeutic agent and protects
CC the therapeutic agent from proteolytic/nucleolytic degradation, from
CC eliciting an immune response, or from rapid renal clearance

XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
|||
Db 4 RRPR 7

RESULT 6
AAY25088
ID AAY25088 standard; peptide; 11 AA.
XX
AC AAY25088;
XX
DT 24-AUG-1999 (first entry)
XX
DE Transduction protein peptide motif 8.
XX
KW Anti-pathogen; fusion protein; protein transduction domain; PTD; AZT;
KW cytotoxic domain; suppressor; infection; medicament; ddI; ddC; d4T; 3TC;
KW FTC; DAPD; 1592U89; CS92; acyclovir; ganciclovir; penciclovir; interferon;
KW apoptosis; virus; HIV; cytomegalovirus; CMV; herpes simplex virus; HSV-1;
KW hepatitis virus; Kaposi's sarcoma-associated herpes virus; KSHV;
KW herpes virus; yellow fever virus; flavivirus; rhinovirus; plasmoidal;
KW transduction efficiency; cytotoxin.
XX
OS Unidentified.
XX
PN WO9929721-A1.
XX
PD 17-JUN-1999.
XX
PF 10-DEC-1998; 98WO-US026358.
XX
PR 10-DEC-1997; 97US-0069012P.
PR 20-APR-1998; 98US-0082402P.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Dowdy SF;
XX
DR WPI; 1999-394958/33.
XX
PT New anti-pathogen systems, particularly for virus and plasmodium
PT infections.
XX
PS Claim 73; Page 90; 123pp; English.
XX
CC This invention describes a novel anti-pathogen system (APS) comprising a
CC fusion protein constructed from a covalently linked protein transduction
CC domain (PTD) and a cytotoxic domain. The APS can be used for suppressing
CC a pathogen infection in a mammal. The method may further comprise
CC administering a medicament e.g. AZT, ddI, ddC, d4T, 3TC, FTC, DAPD,
CC 1592U89, CS92, acyclovir, ganciclovir, penciclovir or an interferon. The
CC APS can also be administered to a mammal in the presence of a pathogen to
CC induce apoptosis in a predetermined population of cells. The products can
CC be used for treating mammals suffering from or susceptible to a viral
CC infection or a disease associated with a virus, e.g. HIV, cytomegalovirus
CC (CMV), herpes simplex virus, e.g. type 1 (HSV-1) hepatitis virus, type C

CC (HCV), Kaposi's sarcoma-associated herpes virus (KSHV or human herpes
CC virus 8), yellow fever virus, flavivirus or rhinovirus, or suffering from
CC or susceptible to plasmodial infection or a disease associated with a
CC plasmodial infection, e.g. *P. falciparum*, *P. vivax*, *P. ovale*, or *P.*
CC *malariae*. The APS exhibits high transduction efficiency and specifically
CC kills or injures cells infected by one or more pathogens. Formation of
CC the cytotoxin is minimized or eliminated in uninfected cells and in
CC infected cells that keep the pathogen inactive. The APS can be
CC specifically tailored to kill or injure cells infected by one or more
CC pathogen strains. This sequence represents a transduction protein motif
CC described in the invention

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
||||
Db 6 RRPR 9

RESULT 7

AAY25086

ID AAY25086 standard; peptide; 11 AA.

XX

AC AAY25086;

XX

DT 24-AUG-1999 (first entry)

XX

DE Transduction protein peptide motif 6.

XX

KW Anti-pathogen; fusion protein; protein transduction domain; PTD; AZT;
KW cytotoxic domain; suppressor; infection; medicament; ddI; ddC; d4T; 3TC;
KW FTC; DAPD; 1592U89; CS92; acyclovir; ganciclovir; penciclovir; interferon;
KW apoptosis; virus; HIV; cytomegalovirus; CMV; herpes simplex virus; HSV-1;
KW hepatitis virus; Kaposi's sarcoma-associated herpes virus; KSHV;
KW herpes virus; yellow fever virus; flavivirus; rhinovirus; plasmodial;
KW transduction efficiency; cytotoxin.

XX

OS Unidentified.

XX

PN WO9929721-A1.

XX

PD 17-JUN-1999.

XX

PF 10-DEC-1998; 98WO-US026358.

XX

PR 10-DEC-1997; 97US-0069012P.

PR 20-APR-1998; 98US-0082402P.

XX

PA (UNIW) UNIV WASHINGTON.

XX

PI Dowdy SF;

XX

DR WPI; 1999-394958/33.

XX
PT New anti-pathogen systems, particularly for virus and plasmodium infections.
XX
PS Claim 73; Page 90; 123pp; English.
XX
CC This invention describes a novel anti-pathogen system (APS) comprising a fusion protein constructed from a covalently linked protein transduction domain (PTD) and a cytotoxic domain. The APS can be used for suppressing a pathogen infection in a mammal. The method may further comprise administering a medicament e.g. AZT, ddI, ddC, d4T, 3TC, FTC, DAPD, 1592U89, CS92, acyclovir, ganciclovir, penciclovir or an interferon. The APS can also be administered to a mammal in the presence of a pathogen to induce apoptosis in a predetermined population of cells. The products can be used for treating mammals suffering from or susceptible to a viral infection or a disease associated with a virus, e.g. HIV, cytomegalovirus (CMV), herpes simplex virus, e.g. type 1 (HSV-1) hepatitis virus, type C (HCV), Kaposi's sarcoma-associated herpes virus (KSHV or human herpes virus 8), yellow fever virus, flavivirus or rhinovirus, or suffering from or susceptible to plasmodial infection or a disease associated with a plasmodial infection, e.g. P. falciparum, P. vivax, P. ovale, or P. malariae. The APS exhibits high transduction efficiency and specifically kills or injures cells infected by one or more pathogens. Formation of the cytotoxin is minimized or eliminated in uninfected cells and in infected cells that keep the pathogen inactive. The APS can be specifically tailored to kill or injure cells infected by one or more pathogen strains. This sequence represents a transduction protein motif described in the invention

XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRRR 11
||||
Db 6 RRPR 9

RESULT 8
AAB26886
ID AAB26886 standard; peptide; 11 AA.
XX
AC AAB26886;
XX
DT 01-FEB-2001 (first entry)
XX
DE PR-39 derived angiogenesis regulatory peptide 2.
XX
KW Angiogenesis; stimulation; PR-39; anoxia; myocardial infarction;
KW myocardial ischaemia; proteasome.
XX
OS Synthetic.
XX
PN WO200057895-A1.
XX

PD 05-OCT-2000.
XX
PF 16-MAR-2000; 2000WO-US007050.
XX
PR 26-MAR-1999; 99US-00276868.
XX
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Simons M, Gao Y;
XX
DR WPI; 2000-628319/60.
XX
PT Stimulating angiogenesis in situ, useful e.g. for treating anoxia and
PT infarction, by administering a PR-39 oligopeptide that regulates
PT enzymatic activity of proteasomes.
XX
PS Claim 13; Page 41; 51pp; English.
XX
CC This invention relates to a method for the stimulation of angiogenesis in
CC situ within a targeted collection of viable cells. The method comprises
CC introducing, into the cytoplasm, at least 1 member of the PR-39
CC oligopeptide collective, which interacts with cytoplasmic proteasomes.
CC Part of the proteolytic activity of the proteasomes is selectively
CC altered so as to stimulate angiogenesis. The method is used to induce
CC angiogenesis in tissue that has suffered anoxia or infarction, e.g.
CC myocardial infarction or chronic myocardial ischaemia, and also to study
CC the mechanisms that control angiogenesis. The present sequence represents
CC a PR-39 derived peptide which interacts with the proteasome and can be
CC used in the method of the invention
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
|||
Db 2 RRPR 5

RESULT 9
AAY93554
ID AAY93554 standard; peptide; 11 AA.
XX
AC AAY93554;
XX
DT 25-SEP-2000 (first entry)
XX
DE Amino acid sequence of a synthetic protein transduction domain.
XX
KW Protein transduction system; protein transduction domain;
KW cytotoxic domain; pathogen infection; retroviral infection;
KW plasmodial infection; cancer; prostate cancer.
XX
OS Synthetic.
XX

PN WO200034308-A2.
XX
PD 15-JUN-2000.
XX
PF 10-DEC-1999; 99WO-US029289.
XX
PR 10-DEC-1998; 98US-0111701P.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Dowdy SF;
XX
DR WPI; 2000-431269/37.
XX
PT Protein transduction system for treating cancer and pathogenic infections
PT has a fusion protein comprising a protein transduction domain covalently
PT linked to a cytotoxic domain.
XX
PS Example 13; Page 85; 127pp; English.
XX
CC AAY93552-57 represent synthetic protein transduction domains, which are
CC used in the protein transduction system of the invention. The
CC specification describes a protein transduction system, which comprises a
CC fusion protein. This fusion protein has a covalently linked protein
CC transduction domain and cytotoxic domain. The system is useful for
CC treating pathogen infection in mammals, infections such as those caused
CC by CMV, HSV-1, HCV, KSHV, yellow fever virus, flavivirus or rhinovirus,
CC retroviral infections such as HIV-1, HIV-2, HTLV-3 and/or LAV, plasmodial
CC infections associated with P.falciparum, P.vivax, P.ovale, P.malariae. It
CC is also useful for treating cancer, especially prostate cancer
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 RRPR 11
Db 6 RRPR 9

RESULT 10
AAY93552
ID AAY93552 standard; peptide; 11 AA.
XX
AC AAY93552;
XX
DT 25-SEP-2000 (first entry)
XX
DE Amino acid sequence of a synthetic protein transduction domain.
XX
KW Protein transduction system; protein transduction domain;
KW cytotoxic domain; pathogen infection; retroviral infection;
KW plasmodial infection; cancer; prostate cancer.
XX
OS Synthetic.

XX
PN WO200034308-A2.
XX
PD 15-JUN-2000.
XX
PF 10-DEC-1999; 99WO-US029289.
XX
PR 10-DEC-1998; 98US-0111701P.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Dowdy SF;
XX
DR WPI; 2000-431269/37.
XX
PT Protein transduction system for treating cancer and pathogenic infections
PT has a fusion protein comprising a protein transduction domain covalently
PT linked to a cytotoxic domain.
XX
PS Example 13; Page 84; 127pp; English.
XX
CC AAY93552-57 represent synthetic protein transduction domains, which are
CC used in the protein transduction system of the invention. The
CC specification describes a protein transduction system, which comprises a
CC fusion protein. This fusion protein has a covalently linked protein
CC transduction domain and cytotoxic domain. The system is useful for
CC treating pathogen infection in mammals, infections such as those caused
CC by CMV, HSV-1, HCV, KSHV, yellow fever virus, flavivirus or rhinovirus,
CC retroviral infections such as HIV-1, HIV-2, HTLV-3 and/or LAV, plasmodial
CC infections associated with *P.falciparum*, *P.vivax*, *P.ovale*, *P.malariae*. It
CC is also useful for treating cancer, especially prostate cancer
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
 ||||
Db 6 RRPR 9

RESULT 11
AAB29435
ID AAB29435 standard; peptide; 11 AA.
XX
AC AAB29435;
XX
DT 09-FEB-2001 (first entry)
XX
DE Synthetic transduction domain, SEQ ID NO:36.
XX
KW Protein transduction domain; fusion molecule; therapeutic agent;
KW drug targetting; drug discovery; cell transduction; bioavailability;
KW vaccine; nervous system disorder; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; pre-senile dementia; epilepsy;

KW seizure; compulsive behaviour; meningitis; encephalitis; ischaemia; spongiform encephalopathy; dyslexia; age-related memory loss; Lou Gehring's disease; viral infection; HIV; bacterial infection.

XX
OS Synthetic.

XX
PN WO200062067-A1.

XX
PD 19-OCT-2000.

XX
PF 28-FEB-2000; 2000WO-US005097.

XX
PR 28-FEB-1999; 99US-0122757P.
PR 29-AUG-1999; 99US-0151291P.

XX
PA (UNIW) UNIV WASHINGTON.

XX
PI Dowdy SF;

XX
DR WPI; 2000-647439/62.

XX
PT Fusion molecules comprising protein transduction domains and therapeutic agents, useful for treating e.g. Alzheimer's and Parkinson's diseases, dementia and epilepsy.

XX
PS Example 13; Page 110; 191pp; English.

CC The invention relates to a novel fusion molecule comprising at least one
CC protein transduction domain (PTD) and at least one linked molecule, where
CC the linked molecule has therapeutic or prophylactic activity against a
CC medical condition. The invention also relates to methods of drug
CC discovery in which the test compound is linked to a suitable transducing
CC protein and introduced to a cell; a method of killing resistant
CC microorganisms using a suitable fusion molecule; a mammal comprising a
CC covalently linked fusion molecule; and a mammal adapted for experimental
CC use in which at least one transduction molecule has been transduced into
CC essentially all the cells of the mammal. The fusion molecule is used to
CC deliver a therapeutic agent to a mammal, especially a human. The linked
CC molecule may be a vaccine, an anti-infective drug, a cardiovascular drug,
CC an antitumour drug, an analgesic, an antiinflammatory, a diagnostic
CC marker or a drug for the treatment or prevention of a central or
CC peripheral nervous system disorder. The central nervous system (CNS)
CC disorder is especially Alzheimer's disease, Parkinson's disease,
CC Huntington's disease, and also includes pre-senile dementia, epilepsy and
CC seizures, compulsive behaviour, meningitis (including viral and bacterial
CC meningitis), encephalitis, ischaemia, scrapie (or related spongiform
CC encephalopathies), dyslexia, age-related memory loss or Lou Gehring's
CC disease. Fusion molecules can also be used to kill virally infected
CC cells, especially those infected with HIV. The vaccines are used to treat
CC or prevent bacterial or viral infections. The methods are a highly
CC effective means for transducing a molecule into an entire mammal or into
CC specific cells, tissues, organs and systems within it. They also overcome
CC bioavailability problems that are associated with many therapeutic agents
CC (e.g., large molecular size, hydrophobicity, hydrophilicity, biological
CC resistance), by providing efficient transduction of the target cell. The
CC present sequence represents a protein transduction domain used in the
CC invention

XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
|||
Db 6 RRPR 9

RESULT 12
AAB29438
ID AAB29438 standard; peptide; 11 AA.
XX
AC AAB29438;
XX
DT 09-FEB-2001 (first entry)
XX
DE Synthetic transduction domain, SEQ ID NO:38.
XX
KW Protein transduction domain; fusion molecule; therapeutic agent;
KW drug targetting; drug discovery; cell transduction; bioavailability;
KW vaccine; nervous system disorder; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; pre-senile dementia; epilepsy;
KW seizure; compulsive behaviour; meningitis; encephalitis; ischaemia;
KW spongiform encephalopathy; dyslexia; age-related memory loss;
KW Lou Gehring's disease; viral infection; HIV; bacterial infection.
XX
OS Synthetic.
XX
PN WO200062067-A1.
XX
PD 19-OCT-2000.
XX
PF 28-FEB-2000; 2000WO-US005097.
XX
PR 28-FEB-1999; 99US-0122757P.
PR 29-AUG-1999; 99US-0151291P.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Dowdy SF;
XX
DR WPI; 2000-647439/62.
XX
PT Fusion molecules comprising protein transduction domains and therapeutic
PT agents, useful for treating e.g. Alzheimer's and Parkinson's diseases,
PT dementia and epilepsy.
XX
PS Claim 38; Page 148; 191pp; English.
XX
CC The invention relates to a novel fusion molecule comprising at least one
CC protein transduction domain (PTD) and at least one linked molecule, where
CC the linked molecule has therapeutic or prophylactic activity against a
CC medical condition. The invention also relates to methods of drug

CC discovery in which the test compound is linked to a suitable transducing
CC protein and introduced to a cell; a method of killing resistant
CC microorganisms using a suitable fusion molecule; a mammal comprising a
CC covalently linked fusion molecule; and a mammal adapted for experimental
CC use in which at least one transduction molecule has been transduced into
CC essentially all the cells of the mammal. The fusion molecule is used to
CC deliver a therapeutic agent to a mammal, especially a human. The linked
CC molecule may be a vaccine, an anti-infective drug, a cardiovascular drug,
CC an antitumour drug, an analgesic, an antiinflammatory, a diagnostic
CC marker or a drug for the treatment or prevention of a central or
CC peripheral nervous system disorder. The central nervous system (CNS)
CC disorder is especially Alzheimer's disease, Parkinson's disease,
CC Huntington's disease, and also includes pre-senile dementia, epilepsy and
CC seizures, compulsive behaviour, meningitis (including viral and bacterial
CC meningitis), encephalitis, ischaemia, scrapie (or related spongiform
CC encephalopathies), dyslexia, age-related memory loss or Lou Gehring's
CC disease. Fusion molecules can also be used to kill virally infected
CC cells, especially those infected with HIV. The vaccines are used to treat
CC or prevent bacterial or viral infections. The methods are a highly
CC effective means for transducing a molecule into an entire mammal or into
CC specific cells, tissues, organs and systems within it. They also overcome
CC bioavailability problems that are associated with many therapeutic agents
CC (e.g., large molecular size, hydrophobicity, hydrophilicity, biological
CC resistance), by providing efficient transduction of the target cell. The
CC present sequence represents a specifically claimed protein transduction
CC domain

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
||||

Db 6 RRPR 9

RESULT 13

AAM97944

ID AAM97944 standard; peptide; 11 AA.

XX

AC AAM97944;

XX

DT 24-JAN-2002 (first entry)

XX

DE Human peptide #1219 encoded by a SNP oligonucleotide.

XX

KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.

XX

OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035498.
XX
PR 28-DEC-1999; 99US-0173419P.
PR 27-DEC-2000; 2000US-00173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
XX
PS Disclosure; Page 3935; 4143pp; English.
XX
CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interferons, interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
||||
Db 7 RRPR 10

RESULT 14
AAE04943
ID AAE04943 standard; peptide; 11 AA.
XX
AC AAE04943;
XX

DT 10-SEP-2001 (first entry)
XX
DE Nuclear Dbf2-related (Ndr) substrate #29.
XX
KW Nuclear Dbf2-related protein kinase; Ndr; cytostatic; gene therapy;
KW calcium binding protein; CBP; tumour; melanoma.
XX
OS Synthetic.
XX
PN US6258776-B1.
XX
PD 10-JUL-2001.
XX
PF 12-AUG-1998; 98US-00133062.
XX
PR 12-AUG-1997; 97GB-00017089.
PR 19-AUG-1997; 97GB-00017499.
XX
PA (NOVS) NOVARTIS AG.
XX
PI Hemmings BA, Millward TA;
XX
DR WPI; 2001-407387/43.
XX
PT Novel composition comprises a peptide comprising part of the sequence of
PT the nuclear Dbf2-related protein kinase, Ndr, useful in treating
PT disorders involving Ndr regulation by CBPs, e.g. melanoma.
XX
PS Example 2; Col 37; 22pp; English.

XX
CC The present peptide sequence is a substrate for Nuclear Dbf2-related
CC protein kinase. The present invention relates to a method of modulating
CC the activity of a protein comprising the activating domain of an Ndr
CC family kinase, by influencing the binding of an EF hand-containing
CC calcium binding protein (CBP). The invention also provides a novel
CC composition comprising nuclear Dbf2-related protein kinase peptides. The
CC composition is useful in treating disorders involving Ndr regulation by
CC CBPs, e.g. tumours especially melanoma. The Ndr protein kinases are also
CC used in gene therapy
XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKTG 7
Db 4 KKTG 7

RESULT 15
AAB97278
ID AAB97278 standard; peptide; 11 AA.
XX
AC AAB97278;
XX

DT 09-AUG-2001 (first entry)
XX
DE PR-39 derived peptide PR-11.
XX
KW PR-39; cathelin; inflammation; wound healing; myocardial infarction;
KW proteasome; proteolysis; alpha7; peptide degradation; angiogenesis;
KW anoxia; chronic myocardial ischaemia; heart tissue.
XX
OS Unidentified.
XX
PN WO200130368-A1.
XX
PD 03-MAY-2001.
XX
PF 06-OCT-2000; 2000WO-US027552.
XX
PR 25-OCT-1999; 99US-00426011.
XX
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Simons M, Gao Y;
XX
DR WPI; 2001-355179/37.
XX
PT Stimulation of angiogenesis and inhibition of proteasome mediated
PT degradation in cells, by introduction of PR-39 oligopeptide or its N-
PT terminal fragments or their conjugates, for use in anoxia and infarction
PT conditions.
XX
PS Claim 13; Page 43; 52pp; English.
XX
CC Peptides AAB97277 - AAB97279 represent PR-39 derived oligopeptides. PR-39
CC is a member of the the cathelin family of proteins, mature PR-39 is 39
CC amino acids in length (see AAB97280), and has been shown to play a role
CC in several inflammatory events including wound healing and myocardial
CC infarction. The PR-39 derived family of oligopeptides cause selective
CC inhibition of proteasome mediated degeneration of peptides and
CC stimulation of angiogenesis after their intracellular introduction to a
CC target cell. PR-39 derived peptides are able to interact with at least
CC the alpha7 subunit of the proteasomes, and therefore alter the
CC proteolytic activity of proteasomes such that a selective increased
CC expression of specific proteins occurs. The invention includes methods
CC for the selective inhibition of proteasome mediated peptide degradation.
CC The method provides means for stimulating angiogenesis as required in
CC living tissues and organs which have suffered defects or have undergone
CC anoxia and/or infarction, myocardial infarction or chronic myocardial
CC ischaemia of heart tissue. Examples are the myocardium, skeletal or
CC smooth muscle, artery or vein, lung, brain, kidney, spleen, liver,
CC gastrointestinal or nerve tissues, limbs, and extremities. A particular
CC example is after myocardial infarction or ischaemia
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
|||
Db 2 RRPR 5

RESULT 16

AAB84692

ID AAB84692 standard; peptide; 11 AA.

XX

AC AAB84692;

XX

DT 17-SEP-2001 (first entry)

XX

DE Amino acid sequence of a PR-39 derived peptide (residues 1-11).

XX

KW PR-39; IkappaBalpa degradation; NFkappaB transcription factor;
KW myocardial infarction; chronic myocardial ischemia; heart disease;
KW anoxia.

XX

OS Unidentified.

XX

PN WO200147540-A1.

XX

PD 05-JUL-2001.

XX

PF 27-DEC-2000; 2000WO-US035293.

XX

PR 29-DEC-1999; 99US-00474967.

XX

PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX

PI Simons M, Gao Y;

XX

DR WPI; 2001-441690/47.

XX

PT Selective inhibition of IkappaBalpa degradation within targeted viable
PT cell collection, involves interacting PR-39 oligopeptide with
PT IkappaBalpa and proteasomes, and altering proteolytic activity of
PT proteasomes.

XX

PS Claim 12; Page 58; 69pp; English.

XX

CC The present sequence represents a PR-39 derived peptide. It is used for
CC selective inhibition of IkappaBalpa degradation within a targeted cell
CC collection in-situ. The method is useful for selectively inhibiting
CC IkappaBalpa protein degradation in situ, decreasing the activity of
CC NFkappaB transcription factor and selective control of NFkappaB-dependent
CC gene expression in situ. The PR-39 derived peptides are useful in the
CC treatment of myocardial infarction, chronic myocardial ischemia of heart
CC disease and anoxia

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
Db 2 RRPR 5

RESULT 17

ABB82469

ID ABB82469 standard; peptide; 11 AA.

XX

AC ABB82469;

XX

DT 22-JAN-2003 (first entry)

XX

DE Peptide fragment comprised in a cell uptake enhancer peptide.

XX

KW Tat; transcompartmental; cytostatic; anti-HIV; therapeutic; diagnostic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal acetylation"

FT Modified-site 10..11

FT /note= "biotinylated"

FT Modified-site 11

FT /note= "C-terminal amide"

XX

PN WO200262396-A2.

XX

PD 15-AUG-2002.

XX

PF 08-FEB-2002; 2002WO-US003819.

XX

PR 08-FEB-2001; 2001US-0267396P.

XX

PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.

PA (PARA/) PARANJP P.

XX

PI Paranjp P, Stein S, Leibowitz MJ, Sinko PJ, Minko T, Williams GC;

PI Zhang G, Pooyan S, Park SH, Qiu B, Ramanathan S;

XX

DR WPI; 2002-713317/77.

XX

PT New transcompartmental delivery promoting composition used for delivering
PT a therapeutic or diagnostic agent comprises a polymer having multiple
PT functional groups, at least one of which is bound to the agent and at
PT least one uptake promoter.

XX

PS Claim 27; Page 106; 142pp; English.

XX

CC The invention relates to a new transcompartmental delivery promoting
CC composition that comprises: (1) polymer (B) having multiple functional
CC groups, at least one which is covalently bound to a therapeutic or
CC diagnostic agent (A), and at one uptake promoter (C) covalently bound to
CC (A); or (2) (B) and at least one (C) bound to (B), where (B) further
CC comprises multiple functional groups at least one of which is covalently

CC bound to (A). The composition is used for delivering a therapeutic or
CC diagnostic agent from an initial bodily compartment (e.g. an
CC extravascular site or an intravascular site) to at least one target
CC bodily compartment (e.g. circulation, central nervous system, brain, eye
CC or an intracellular environment (including an epithelial cell, an
CC endothelial cell, a phagocytic cell, a lymphocyte, a neuron or a cancer
CC cell); and for delivering therapeutic or diagnostic agent such as
CC macrophages for the treatment of HIV infection. Sequences ABB82464-470
CC represent specific examples of peptide fragments contained in the
CC therapeutic agent or uptake enhancer comprising a thiol compound
XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
||||
Db 4 RRPR 7

RESULT 18
ABP54091
ID ABP54091 standard; peptide; 11 AA.
XX
AC ABP54091;
XX
DT 15-JAN-2003 (first entry)
XX
DE Transport moiety cellular uptake peptide #15.
XX
KW Transporter; Spaced arginine moiety; vasotropic; neuroleptic; analgesic;
KW antiparkinsonian; biologically active compound; biological membrane;
KW epithelial tissue; endothelial tissue; ischaemia; neurotransmitter;
KW schizophrenia; Parkinson's disease; pain; transport moiety.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /label= Acp
FT /note= "epsilon-aminocaproic acid (aca); N-terminally
FT modified with fluorescein (Fl)"
FT Modified-site 11
FT /note= "C-terminally modified with CONH2"
XX
PN WO200265986-A2.
XX
PD 29-AUG-2002.
XX
PF 14-FEB-2002; 2002WO-US004491.
XX
PR 16-FEB-2001; 2001US-00269627.
XX
PA (CELL-) CELLGATE INC.
XX

PI Wender PA, Rothbard JB, Wright L, Kreider EL, Vandeusen CL;
XX
DR WPI; 2002-740700/80.
XX
PT Composition, useful for increasing the transport of a biologically active
PT compound across a biological membrane, comprises a biologically active
PT compound and a transport moiety.
XX
PS Example 1; Page 24; 58pp; English.
XX
CC The present invention describes a composition (C) comprising a
CC biologically active compound (A) and a transport moiety (B) of formula:
CC $(ZY_2)_nZ$ (I), $(ZY)_nZ$ (II), $(ZYY)_nZ$ (III) or $(ZYYY)_nZ$ (IV), where Z = L-
CC arginine or D-arginine; Y = amino acid (not comprising amidino or
CC guanidino moiety); and n = 2-10. Also described is a method for
CC increasing the transport of a biologically active compound across a
CC biological membrane involving administering (C). (C) has vasotropic,
CC neuroleptic, antiparkinsonian and analgesic activities. (C) is used for
CC increasing the transport of a biologically active compound across a
CC biological membrane and across and into animal epithelial or endothelial
CC tissues. (C) can be used for treating ischaemia and delivering
CC neurotransmitters and other agents for treating schizophrenia,
CC Parkinson's disease and pain. The transport of the biologically active
CC compound across the biological membrane is increased relative to the
CC transport of the biologically active compound in the absence of the
CC transport moiety. The present sequence represents a transport moiety
CC cellular uptake peptide, which is used in an example from the present
CC invention
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
||||
Db 4 RRPR 7

RESULT 19
ABO14954
ID ABO14954 standard; peptide; 11 AA.
XX
AC ABO14954;
XX
DT 22-AUG-2003 (first entry)
XX
DE Microsomal delta-12 desaturase related peptide #29.
XX
KW Microsomal fatty acid delta-12 desaturase; ricinoleic acid;
KW palmitic acid; stearic acid; unsaturated fatty acid;
KW coronary heart disease.
XX
OS Unidentified.
XX
PN US2003033633-A1.

XX
PD 13-FEB-2003.
XX
PF 28-MAR-2002; 2002US-00108795.
XX
PR 17-NOV-1992; 92US-00977339.
PR 15-OCT-1993; 93WO-US009987.
PR 20-JUN-1994; 94US-00262401.
PR 14-AUG-1998; 98US-00133962.
PR 26-OCT-2000; 2000US-00697374.
XX
PA (LIGH/) LIGHTNER J E.
PA (OKUL/) OKULEY J J.
PA (HITZ/) HITZ W D.
PA (KINN/) KINNEY A J.
PA (YADA/) YADAV N.
PA (GRAU/) PEREZ GRAU L.
XX
PI Lightner JE, Okuley JJ, Hitz WD, Kinney AJ, Yadav N;
PI Perez Grau L;
XX
DR WPI; 2003-479605/45.
XX
PT New nucleic acid fragment encoding a fatty acid desaturase or a fatty acid desaturase-related enzyme, useful for producing transgenic plants with altered levels of unsaturated fatty acids, plant genetic mapping and breeding programs.
XX
PS Disclosure; Page 41; 44pp; English.
XX
CC The invention relates to an isolated nucleic acid fragment encoding a microsomal delta-12 fatty acid desaturase or a fatty acid desaturase-related enzyme that is at least 50 % identical to a polypeptide of P1-P6 (not shown in the specification). Also included are an isolated nucleic acid fragment comprising a sequence encoding a delta-12 fatty acid hydroxylase, a chimaeric gene capable of causing altered levels of ricinoleic acid or fatty acids in a transformed plant cell (comprising the nucleic acid fragment that is operably linked to suitable regulatory sequences), a plant containing the chimaeric gene, oils obtained from the seeds of the plant, producing seed oil containing altered levels of unsaturated fatty acids, molecular breeding to obtain altered levels of fatty acid in seed oil of oil-producing plant species, restriction fragment length polymorphism (RFLP) mapping of the nucleic acids, isolating nucleic acid fragments encoding fatty acid desaturases and related enzymes, altering fatty acid composition in seeds, reducing polyunsaturated fatty acids in rapeseed or soybean oil, reducing saturated fatty acids in rapeseed oil, a Brassica spp. (plant with seed palmitic acid of 2.7 % or seed stearic acid of 1.1%, or lower of total fatty acid), a Brassica spp. plant (with a combined palmitic acid and stearic acid content of 3.9% or lower of total fatty acids), a soybean plant (with seed palmitic acid of 6.7% or seed stearic acid content of 2.1%, or lower of total fatty acid), a soybean plant (with a combined seed palmitic acid and stearic acid content of 9.2% or lower of total fatty acids) and oils obtained from the plants above. The nucleic acid fragments and chimeric genes are useful for producing transgenic plants with altered levels of unsaturated fatty acids. The chimeric genes are useful for transforming various plants to modify the fatty acid

CC composition of the plant or the oil produced by the plant. The nucleic
CC acid fragments are also useful as RFLP fragments in plant genetic mapping
CC and plant breeding programs. Production of plant oil for human
CC consumption with higher mono-unsaturated fat content and a lower
CC saturated fat content may reduce the incidence of coronary heart disease.
CC The present sequence is a delta-12 desaturase associated peptide. Note:
CC The disclosure states that SEQ ID 1-12 are cDNAs and their encoded
CC desaturase proteins (these are claimed). The sequence listing only
CC contains 34 short peptide sequences which are obviously not the claimed
CC cDNAs or full length proteins. It appears that the sequence listing is
CC that of an unrelated patent and has been substituted in error
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKTG 7
||||
Db 4 KKTG 7

RESULT 20
ABP60206
ID ABP60206 standard; peptide; 11 AA.
XX
AC ABP60206;
XX
DT 14-FEB-2003 (first entry)
XX
DE Synthetic peptide 5.
XX
KW Substrate specificity; enzyme activity; microarray; diagnosis; cancer;
KW differential analysis; high throughput analysis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..2
FT /note= "Optionally absent"
FT Modified-site 2
FT /label= bAla
FT Modified-site 11
FT /note= "C-terminal amide"
XX
PN WO200283933-A2.
XX
PD 24-OCT-2002.
XX
PF 17-APR-2002; 2002WO-EP004265.
XX
PR 17-APR-2001; 2001DE-01018774.
XX
PA (JERI-) JERINI AG.
XX
PI Schneider-Mergener J, Schutkowski M, Reimer U, Dong L, Panse S;

PI Scharn D, Osterkamp F, Hummel G, Jobron L;
XX
DR WPI; 2003-075559/07.
XX
PT Determining substrate specificity of enzymes, useful e.g. in screening
PT for modulators, by detecting molecular weight changes in ordered array of
PT amino acid sequences.
XX
PS Example 18; Fig 8D; 79pp; German.
XX
CC The invention relates to determining the substrate specificity of an
CC enzymatic activity (EA) by contact and/or incubation of EA with an array
CC of many amino acid sequences (I) immobilised, in a directed manner, on
CC the flat surface of a carrier then detecting reaction of (I) with EA,
CC where the reaction is monitored from a change in the molecular weight of
CC (I). The method is used to determine the pattern of EA in a sample, e.g.
CC for differential analysis; for identification of a strain or species and
CC for diagnosis of disease, e.g. cancer. It can also be used for selection
CC of active agents, i.e. compounds that modulate EA. The method is suitable
CC for high throughput testing and the use of a non-porous carrier surface
CC makes it possible to use extremely small quantities of EA or sample. The
CC signal-to-noise ratio is much lower (typically by a factor of 3000) than
CC that in conventional peptide/protein arrays. The present sequence is that
CC of a peptide used in examples of the invention
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGRR 9
||||
Db 5 TGRR 8

RESULT 21
ABP56088
ID ABP56088 standard; peptide; 11 AA.
XX
AC ABP56088;
XX
DT 27-FEB-2003 (first entry)
XX
DE Protein transduction domain (PTD) peptide #10.
XX
KW Cancer cell death; cancer; tumour; protein transduction domain; CAV;
KW chicken anaemia virus; cytostatic; proliferative cell disorder;
KW carcinogenesis; metastasis.
XX
OS Unidentified.
XX
PN WO200285305-A2.
XX
PD 31-OCT-2002.
XX
PF 24-APR-2002; 2002WO-US013092.

XX
PR 24-APR-2001; 2001US-0286099P.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Dowdy SF, Ezhevsky SA, Wadia JS;
XX
DR WPI; 2003-093056/08.
XX
PT Novel fusion molecule useful for preventing or treating cancer, comprises
PT a protein transduction domain and a chicken anemia virus VP3 molecule.
XX
PS Claim 26; Page 68; 104pp; English.
XX
CC The present invention describes a fusion molecule (I) comprising at least
CC one protein transduction domain (PTD) and at least one chicken anaemia
CC virus (CAV) VP3 molecule. (I) has cytostatic activity and can be used for
CC inducing cell death. (I) is useful for detecting cancerous or pre-
CC cancerous cells in a mammal or for killing or injuring cancerous or pre-
CC cancerous cells in a mammal. (I) is useful as a magnetic bullet to
CC selectively kill cancer cells in vitro and in vivo, for inducing cell
CC death, and for preventing or treating cancer and related proliferative
CC disorders. (I) is also useful for studying mechanisms of carcinogenesis
CC and metastases eukaryotic cells. (I) effectively transduces VP3 molecules
CC directly into the cells. (I) attacks cancer and pre-cancerous cells while
CC leaving normal cells relatively unharmed. Since more cells can be
CC targeted by (I) when compared with past attempts using different VP3
CC constructs, potential for patient relapse and side-effects are greatly
CC reduced. The present sequence represents a specifically claimed PTD
CC peptide which is given in the exemplification of the present invention
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 11
|||
Db 6 RRP 9

RESULT 22
ABG33050
ID ABG33050 standard; peptide; 11 AA.
XX
AC ABG33050;
XX
DT 23-JAN-2003 (first entry)
XX
DE Pig arg/pro rich peptide PR-11.
XX
KW Pig; hypoxia inducible factor 2 alpha; HIF-2alpha; RDS;
KW neonatal respiratory distress syndrome; pulmonary hypertension;
KW hypoxia induced disorder; bronchopulmonary dysplasia; VEGF;
KW chronic lung disease of prematurity; vascular endothelial growth factor;
KW arg/pro rich peptide; PR-11.

XX
OS Sus scrofa.
XX
PN WO200286497-A2.
XX
PD 31-OCT-2002.
XX
PF 24-APR-2002; 2002WO-EP004479.
XX
PR 24-APR-2001; 2001EP-00201481.
PR 10-AUG-2001; 2001EP-00203073.
PR 11-JAN-2002; 2002EP-00075077.
XX
PA (VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
PA (COLL-) COLLEN RES FOUND D.
XX
PI Compernolle V, Carmeliet P;
XX
DR WPI; 2003-058742/05.
XX
PT Use of hypoxia inducible factor 2 alpha to screen inhibitors of pulmonary hypertension, comprises incubating the factor and the inhibitor, isolating inhibitor and determining ability of inhibitor to inhibit hypertension.
XX
PS Disclosure; Page 16; 57pp; English.
XX
CC The invention relates to the use of Hypoxia inducible factor 2 alpha (HIF-2alpha) as a target to screen for molecules that are able to inhibit the development of pulmonary hypertension, comprising incubating a mixture comprising HIF-2alpha and at least one molecule, allowing binding between HIF-2alpha and the molecule, isolating the molecule binding to HIF-2alpha, and determining the ability of the molecule to inhibit the development of pulmonary hypertension; or incubating a mixture comprising HIF-2 alpha, a reporter construct (where the reporter gene is driven by HIF-2alpha) and at least one molecule, determining if the latter incubation resulted in at least 50% reduction in expression of the reporter gene, and determining the ability of the molecule to inhibit the development of pulmonary hypertension. Also included are producing a pharmaceutical composition comprising the inhibitor identified using HIF-2alpha and further mixing the inhibitor (its derivative or homologue) with a carrier and use of HIF-2alpha or vascular endothelial growth factor (VEGF) (or their fragment or homologue) for manufacturing a medicament for treating neonatal respiratory distress syndrome (RDS). HIF-2alpha is useful for screening molecules that inhibit the development of pulmonary hypertension. HIF-2alpha and VEGF are useful for manufacturing a medicament for treating neonatal respiratory distress syndrome (a hypoxia induced disorder which also includes bronchopulmonary dysplasia and chronic lung disease of prematurity. The present sequence is a Pig arg/pro rich peptide, PR-11, which is active against RDS
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
|||
Db 2 RRPR 5

RESULT 23

ABU63113

ID ABU63113 standard; peptide; 11 AA.

XX

AC ABU63113;

XX

DT 24-SEP-2003 (first entry)

XX

DE Microsomal delta-12 fatty acid desaturase associated peptide #29.

XX

KW Microsomal delta-12 fatty acid desaturase; desaturase-related enzyme;
KW transgenic plant; unsaturated fatty acid.

XX

OS Synthetic.

XX

PN US2003066104-A1.

XX

PD 03-APR-2003.

XX

PF 03-APR-2002; 2002US-00115364.

XX

PR 17-NOV-1992; 92US-00977339.

PR 15-OCT-1993; 93WO-US009987.

PR 20-JUN-1994; 94US-00262401.

PR 14-AUG-1998; 98US-00133962.

PR 26-OCT-2000; 2000US-00697379.

XX

PA (LIGH//) LIGHTNER J E.

PA (OKUL//) OKULEY J J.

PA (HITZ//) HITZ W D.

PA (KINN//) KINNEY A J.

PA (YADA//) YADAV N.

PA (GRAU//) PEREZ GRAU L.

XX

PI Lightner JE, Okuley JJ, Hitz WD, Kinney AJ, Yadav N;

PI Perez Grau L;

XX

DR WPI; 2003-540829/51.

XX

PT New nucleic acid fragment comprising a sequence encoding a fatty acid
PT desaturase or desaturase-related enzyme, useful for creating transgenic
PT plants with altered levels of unsaturated fatty acids.

XX

PS Disclosure; Page 40; 44pp; English.

XX

CC The invention describes a new isolated nucleic acid fragment comprising a
CC sequence encoding a fatty acid desaturase or desaturase-related enzyme
CC with at least 50% identity to the polypeptide encoded by the seven amino
CC acid sequences comprising 9-10 aa residues. The nucleic acid fragment is
CC useful for creating transgenic plants with altered levels of unsaturated
CC fatty acids. This is the amino acid sequence of a microsomal delta-12
CC fatty acid desaturase associated peptide. Note: The sequence listing

CC given in the specification does not appear to correspond to the sequences

CC described in the specification

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKTG 7
||||
Db 4 KKTG 7

RESULT 24

ADB87318

ID ADB87318 standard; peptide; 11 AA.

XX

AC ADB87318;

XX

DT 04-DEC-2003 (first entry)

XX

DE Human peptide P11 related to post-operative adhesion treatment.

XX

KW hypoxia-induced gene; adhesion formation; hypoxia inducible factor;
KW placental growth factor; PlGF; vascular endothelial growth factor-B;
KW VEGF-B; post-operative adhesions; POA; surgery; gynaecological surgery;
KW pelvic surgery; cardiological surgery; surgical trauma; scar formation;
KW post-operative morbidity; post-operative mortality; vulnerability;
KW gene therapy; wound; inflammation; trauma; intestinal obstruction;
KW small bowel obstruction; chronic pelvic pain; infertility; PR11; PR39;
KW human.

XX

OS Homo sapiens.

XX

PN WO2003063904-A2.

XX

PD 07-AUG-2003.

XX

PF 29-JAN-2003; 2003WO-EP000892.

XX

PR 29-JAN-2002; 2002GB-00001983.

PR 04-FEB-2002; 2002GB-00002379.

PR 29-OCT-2002; 2002GB-00025128.

XX

PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

PA (THRO-) THROMB-X.

PA (LEUV-) LEUVEN RES & DEV.

XX

PI Koninckx P, Carmeliet P, Collen D, Molinas Sanabria CR;

XX

DR WPI; 2003-646103/61.

XX

PT New inhibitors of hypoxia-induced gene (e.g. hypoxia inducible factor,
PT placental growth factor, or vascular endothelial growth factor-B gene),
PT useful for treating adhesion formation resulting from wounds, surgery or
PT inflammation.

XX

PS Claim 5; Page 7; 33pp; English.

XX

CC This invention relates to a novel compound that inhibits the expression
CC and/or activity of a hypoxia-induced gene used for the manufacture of a
CC medicament for treating adhesion formation. The hypoxia-induced gene is a
CC hypoxia inducible factor, placental growth factor (PIGF), or vascular
CC endothelial growth factor-B (VEGF-B). Post-operative adhesions (POA) are
CC an unwanted result from surgery (for example gynaecological, pelvic or
CC cardiological surgery), when surgical trauma to tissue often causes
CC permanent scar formation which connects the tissue to another organ, and
CC are a major source of post-operative morbidity and mortality. No single
CC therapeutic approach has, to date, proven universally effective in
CC preventing formation of post-operative adhesion formation. The invention
CC may have vulnerary activity and may be useful in both humans and veterinary
CC applications for the treatment of adhesion formation by gene therapy. The
CC compound is useful for treating adhesion formation, or for manufacturing
CC a medicament for treating adhesion formation that results from wound,
CC surgery, inflammation or trauma. In particular, the compound may be
CC useful for preventing, suppressing, ameliorating and/or treating post-
CC operative/post-wounding adhesions formations, which may result in
CC intestinal obstructions, small bowel obstructions, chronic pelvic pain,
CC or infertility in women. The present sequence is the amino acid sequence
CC of peptide PR11, a truncated form of hypoxia inducible factor protein
CC PR39, which is preferred for the creation of the medicaments of the
CC invention.

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
||||

Db 2 RRPR 5

RESULT 25

ADC19836

ID ADC19836 standard; peptide; 11 AA.

XX

AC ADC19836;

XX

DT 18-DEC-2003 (first entry)

XX

DE Fluorescently labelled spaced arginine transport peptide #16.

XX

KW Cellular membrane transport peptide; epithelial tissue;
KW endothelial tissue; drugs transport; stratum corneum; antibacterial;
KW antifungal; antiviral; antiproliferative; immunosuppressive; vitamin;
KW analgesic; hormone.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /label
FT /note= "Xaa is fluorescently labelled epsilon-
FT aminocaprianoic acid"
FT Modified-site 11
FT /label= OTHER
FT /note= "Arg is covalently bound to a CONH₂ group"
XX
PN US2003032593-A1.
XX
PD 13-FEB-2003.
XX
PF 14-FEB-2002; 2002US-00078247.
XX
PR 16-FEB-2001; 2001US-0269627P.
XX
PA (CELL-) CELLGATE INC.
XX
PI Wender PA, Rothbard JB, Wright L, Kreider EL, Vandeusen CJ;
XX
DR WPI; 2003-786846/74.
XX
PT Composition used for increasing transport of biologically active compound
PT across biological membrane comprises biologically active compound and
PT transport group.
XX
PS Example 1; Page 9; 33pp; English.
XX
CC The invention relates to a composition comprising a biologically active
CC compound and a transport group. The transport group comprises a spaced
CC poly-Arginine based peptide of formula given in the specification. The
CC spaced poly-Arginine based peptide acts as a cellular membrane transport
CC signal and effects transport of the biologically active compound across
CC the membrane. The conjugate is also useful in therapeutic, prophylactic
CC and diagnostic applications. The composition improves the transport of
CC biologically active compounds across the biological membrane and into
CC animal epithelial or endothelial tissues. The arginine residue of the
CC conjugate provides an enhanced transport of drugs and are a part of the
CC polypeptide that provides suitable spacing between arginine residues. The
CC transport groups deliver an agent across the stratum corneum, which
CC previously had been a nearly impenetrable barrier to drug delivery. The
CC ability of the conjugate to obtain penetration of skin layers improves
CC the efficacy of compounds such as antibacterials, antifungals,
CC antivirals, antiproliferatives, immunosuppressives, vitamins, analgesics
CC and hormones. The present sequence is a Fluorescently labelled spaced
CC arginine transport peptide of the invention.
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 RRPR 11
Db 4 RRPR 7

RESULT 26
ADC03321
ID ADC03321 standard; peptide; 11 AA.
XX
AC ADC03321;
XX
DT 18-DEC-2003 (first entry)
XX
DE Synthetic internal peptide #29.
XX
KW fatty acid desaturase; ricinoleic acid; plant oil;
KW plant lipid composition; fatty acid composition;
KW saturated fatty acid reduction; unsaturated fatty acid reduction;
KW rapeseed oil; soybean oil.
XX
OS Synthetic.
XX
PN US2003074694-A1.
XX
PD 17-APR-2003.
XX
PF 03-APR-2002; 2002US-00115365.
XX
PR 17-NOV-1992; 92US-00977339.
PR 15-OCT-1993; 93WO-US009987.
PR 20-JUN-1994; 94US-00262401.
PR 14-AUG-1998; 98US-00133962.
PR 26-OCT-2000; 2000US-00697374.
XX
PA (LIGH/) LIGHTNER J E.
PA (OKUL/) OKULEY J J.
PA (HITZ/) HITZ W D.
PA (KINN/) KINNEY A J.
PA (YADA/) YADAV N.
PA (GRAU/) PEREZ GRAU L.
XX
PI Lightner JE, Okuley JJ, Hitz WD, Kinney AJ, Yadav N;
PI Perez Grau L;
XX
DR WPI; 2003-615971/58.
XX
PT New isolated nucleic acid fragment comprising a sequence encoding a fatty
PT acid desaturase or fatty acid desaturase-related enzyme, useful for
PT altering fatty acid compositions in rapeseed or soybean plants.
XX
PS Disclosure; Page 40; 44pp; English.
XX
CC The invention relates to an isolated nucleic acid fragment comprising a
CC sequence encoding a fatty acid desaturase or fatty acid desaturase-
CC related enzyme. The nucleic acid fragment is useful for making a chimeric
CC gene capable of causing altered levels of ricinoleic acid in a
CC transformed plant cell, plants containing the chimeric genes, oil
CC obtained from the seeds of the plant, RFLP mapping, isolating nucleic
CC acid fragments encoding fatty acid desaturases and related enzymes. The
CC nucleic acid fragments are useful for altering plant lipid compositions,
CC particularly fatty acid compositions by reducing saturated or unsaturated
CC fatty acids in rapeseed or soybean oils. The present sequence represents

CC a synthetic internal peptide of the invention.

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKTG 7
||||
Db 4 KKTG 7

RESULT 27

AAP40439

ID AAP40439 standard; peptide; 11 AA.

XX

AC AAP40439;

XX

DT 25-MAR-2003 (revised)

DT 03-OCT-2002 (revised)

DT 14-FEB-1992 (first entry)

XX

DE Sequence of peptide with immunomodulating activity.

XX

KW Immunopotentiator; antimicrobial; antiviral; immunomodulator.

XX

OS Synthetic.

XX

PN EP103858-A.

XX

PD 28-MAR-1984.

XX

PF 16-SEP-1983; 83EP-00109147.

XX

PR 17-SEP-1982; 82JP-00162873.

PR 25-NOV-1982; 82JP-00207335.

XX

PA (FUJI) FUJISAWA PHARM CO LTD.

XX

PI Hashimoto M, Hemmi K;

XX

DR WPI; 1984-083584/14.

XX

PT Penta- to tri-deca:peptide(s) - useful as strong immuno-potentiators esp.
PT against microbes and viruses.

XX

PS Claim 1; Page 82; 87pp; English.

XX

CC The first AA of each claimed peptide is bonded to H and the final AA is
CC bonded to OH. The peptides are useful as antimicrobial and antiviral
CC agents. Dose is 0.1-1000 mg/kg. daily. (Updated on 03-OCT-2002 to add
CC missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKT 6
|||
Db 5 KKT 7

RESULT 28

AAP50159

ID AAP50159 standard; protein; 11 AA.

XX

AC AAP50159;

XX

DT 30-NOV-1991 (first entry)

XX

DE Human interferon-gamma (gamma-IFN) peptide corresp. to a slab SDS-PAGE
DE mol. wt. of 26,000 +/- 3000 daltons.

XX

KW Gamma-interferon; virucide; antitumour; immunostimulant.

XX

OS Homo sapiens.

XX

PN EP137691-A.

XX

PD 17-APR-1985.

XX

PF 28-AUG-1984; 84EP-00305859.

XX

PR 29-AUG-1983; 83US-00527209.

XX

PA (MELO-) MELOY LAB INC.

PA (MERO-) MEROY LAB INC.

XX

PI Braude IA;

XX

DR WPI; 1985-094592/16.

XX

PT Homogeneous human interferon-gamma - obtd. by incubation of leukocytes,
PT inducer and modulator for inducer.

XX

PS Claim 10; Page 53; 59pp; English.

XX

CC The inventors claim a method for the production of gamma-IFN by
CC incubation of leukocytes, inducer and modulator for inducer. They also
CC claim species of homogeneous human interferon-gamma characterised by the
CC partial AA sequences in AAP50157 or AAP50159

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KTG 7
|||
Db 8 KTG 10

RESULT 29
AAP82336
ID AAP82336 standard; peptide; 11 AA.
XX
AC AAP82336;
XX
DT 13-NOV-1990 (first entry)
XX
DE Compound in vaccine against Plasmodium falciparum malaria (Formula I).
XX
KW Malaria vaccines; polymers; Plasmodium falciparum; asexual blood stage;
KW human parasite.
XX
OS Synthetic.
XX
PN EP275196-A.
XX
PD 20-JUL-1988.
XX
PF 13-JAN-1988; 88EP-00300262.
XX
PR 14-JAN-1987; 87US-00003194.
PR 29-DEC-1987; 87US-00135027.
XX
PA (PATA/) PATARROYO M E.
XX
PI Patarroyo ME;
XX
DR WPI; 1988-199632/29.
XX
PT New peptide(s) and peptide polymers - useful for prodn. of malaria
PT vaccines.
XX
PS Claim 15 (I); Page 13; 13pp; English.
XX
CC The peptide is a vaccine component against the asexual blood stage of the
CC malaria parasite. It is the synthetic hybrid protein SPf 35.1 peptide of
CC 8 amino acids except for the absence of the first three residues. The
CC peptide is an alpha hydrophilic structure, and the compound even on its
CC own elicits antibodies delaying the appearance of parasitaemia in some
CC vaccinated animals. Mixtures of the peptides of AAP82336-P82340 provide
CC complete immunity
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NKK 5
|||
Db 6 NKK 8

RESULT 30

AAP82811
ID AAP82811 standard; peptide; 11 AA.
XX
AC AAP82811;
XX
DT 06-DEC-1990 (first entry)
XX
DE Peptide fragment of Plasmodium proteins used in antimalaria vaccines (I).
XX
KW Plasmodium; antimalarial vaccine; parasite.
XX
OS Synthetic.
XX
PN US4735799-A.
XX
PD 05-APR-1988.
XX
PF 14-JAN-1987; 87US-00003194.
XX
PR 29-DEC-1987; 87US-00135027.
XX
PA (PATA/) PATARROYO M E.
XX
PI Patarroyo ME;
XX
DR WPI; 1988-112448/16.
XX
PT New peptide fragments of Plasmodium proteins - useful for prodn. of
PT antimalarial vaccines.
XX
PS Claim 1; Page 9; 6pp; English.
XX
CC This peptide is an alpha hydrophilic structure corresponding to the amino
CC terminal parts of the protein molecule 35 kD. Vaccines contain (I), (II)
CC and (III); AAP82811, AAP82812 and AAP82812 resp; in a wt. ratio of (1-
CC 10):(1-10):(1-10), esp. 1:1:1, in normal saline soln. or squalene.
CC Immunogenic activity may be increased by coupling (I)-(III) to bovine
CC serum albumin with gluteraldehyde or by coupling (I)-(III) by
CC copolymerisation. The peptides (I)-(V); AAP82811-15; provide partial
CC immunity to malaria caused by Plasmodium falciparum. Combinations of (I)-
CC (III) provide complete immunity in Aotos monkeys
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NKK 5
|||
Db 6 NKK 8

RESULT 31
AAP90842
ID AAP90842 standard; protein; 11 AA.
XX

AC AAP90842;

XX

DT 25-MAR-2003 (revised)

DT 31-OCT-2002 (revised)

DT 29-JUN-1990 (first entry)

XX

DE New bradykinin analogue with D-Arg, Hyp, beta-(2-thienyl)-Ala and D-Phe.

XX

KW Bradykinin analogue; bradykinin antagonist.

XX

OS Mammalia.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1
/label= D-Arg

FT Misc-difference 3
/label= Hyp

FT Misc-difference 5
/label= OTHER
/note= "beta-(2-thienyl)-Ala"

FT Misc-difference 7..7
/label= D-Phe

FT Misc-difference 8
/label= OTHER
/note= "As above"

XX

PN WO8901781-A.

XX

PD 09-MAR-1989.

XX

PF 29-AUG-1988; 88WO-US002960.

XX

PR 02-SEP-1987; 87US-00091995.

XX

PA (STEW/) STEWART J M.

PA (NOVA-) NOVA TECHN LTD.

PA (NOVA-) NOVA TECHN LTD.

XX

PI Stewart JM, Vavrek RJ;

XX

DR WPI; 1989-085401/11.

XX

PT New peptide bradykinin analogues - with D-amino acid in 7 position,

PT useful as bradykinin antagonists.

XX

PS Claim 26; Page 55; 54pp; English.

XX

CC It may be prep'd. by conventional liq. - or solid-phase peptide synthesis
CC methods. It is useful for treating local pain, inflammation and swelling,
CC rhinitis, hypotension, asthma, arthritis, diarrhoea, irritable bowel
CC syndrome, carcinoid syndrome, angina pain, and anaphylactic or septic
CC shock. Pharmaceutical compsns. can be made with it. (Updated on 31-OCT-
CC 2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA
CC field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 1 RRP 3

RESULT 32

AAP90643

ID AAP90643 standard; protein; 11 AA.

XX

AC AAP90643;

XX

DT 10-MAR-2003 (revised)

DT 09-AUG-1990 (first entry)

XX

DE Signal peptide NOS Synthetic.

XX

KW NOS; signal peptide; nucleolus.

XX

OS Unidentified.

XX

PN JP01096196-A.

XX

PD 14-APR-1989.

XX

PF 08-OCT-1987; 87JP-00252377.

XX

PR 08-OCT-1987; 87JP-00252377.

XX

PA (HATA/) HATANAKA S.

XX

DR WPI; 1989-155085/21.

XX

PT New peptide NOS having specific aminoacid sequence - used to localise
PT protein in nucleolus.

XX

PS Claim 1; Page 1; 12pp; Japanese.

XX

CC The peptide is useful for localising a protein in the nucleolus. DNA
CC encoding it is inserted downstream of promoter in a plasmid to give pNOS
CC Synthetic. DNA encoding an opt protein is also ligated into the vector,
CC and the pNOS introduced to a host (eg E.coli). Plasmid DNA is then
CC extracted from the cells and transfected into eukaryotic cells which have
CC a nucleolus. Protein localisation can be detected immunologically within
CC hours. See also AAP90642-4. (Updated on 10-MAR-2003 to add missing OS
CC field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 8 RRP 10

RESULT 33

AAR09490

ID AAR09490 standard; peptide; 11 AA.

XX

AC AAR09490;

XX

DT 25-MAR-2003 (revised)

DT 17-JUN-1993 (first entry)

XX

DE Bradykinin antagonist having D-Tic (41).

XX

KW 1,2,3,4-tetrahydroisoquinoline-3-ylcarbonyl; wound; burns; erythema;

KW oedema; angina; asthma; allergy; inflammation; hypotension.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1

FT /note= "D-form residue"

FT Modified-site 3

FT /note= "hydroxyproline"

FT Modified-site 6

FT /label= OTHER

FT /note= "2-thienylalanyl"

FT Modified-site 8

FT /label= OTHER

FT /note= "D-tetrahydroisoquinoline-3-ylcarbonyl"

XX

PN EP370453-A.

XX

PD 30-MAY-1990.

XX

PF 21-NOV-1989; 89EP-00121498.

XX

PR 19-MAY-1989; 89DE-03916291.

PR 03-JUN-1989; 89DE-03918225.

XX

PA (FARH) HOECHST AG.

XX

PI Henke S, Anagnostop H, Breipohl G, Knolle J, Stechel J;

PI Scholkens B, Fehihaber HW;

XX

DR WPI; 1990-165194/22.

XX

PT New oligopeptide with tetra:hydro:isoquinoline-carboxylic acid residue -

PT antagonists of bradykinin, for treating e.g. wounds, asthma, allergy,

PT hypotension, etc.

XX

PS Example 41; Page 16; 34pp; German.

XX

CC The peptide is a bradykinin antagonist, so is useful for treating any
CC condition where bradykinin or its analogues are involved, e.g. wounds,

CC burns, erythema, oedema, angina, asthma, allergy, inflammation,
CC hypotension, etc. Compsns. for topical application or inhalation contain
CC 0.01-5 mg/ml and the systemic dose is 0.01-10 mg/ml. (Updated on 25-MAR-
CC 2003 to correct PI field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||

Db 1 RRP 3

RESULT 34

AAR09489

ID AAR09489 standard; peptide; 11 AA.

XX

AC AAR09489;

XX

DT 25-MAR-2003 (revised)

DT 17-JUN-1993 (first entry)

XX

DE Bradykinin antagonist having D-Tic (40).

XX

KW 1,2,3,4-tetrahydroisoquinoline-3-ylcarbonyl; wound; burns; erythema;

KW oedema; angina; asthma; allergy; inflammation; hypotension.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1

FT /note= "D-form residue"

FT Modified-site 4

FT /note= "hydroxyproline"

FT Modified-site 6

FT /label= OTHER

FT /note= "2-thienylalanyl"

FT Modified-site 8

FT /label= bALA

FT Modified-site 9

FT /label= OTHER

FT /note= "D-tetrahydroisoquinoline-3-ylcarbonyl"

FT Modified-site 10

FT /label= OTHER

FT /note= "cis,endo-2-azabicyclo[3.3.0]octane -3-S-carbonyl"

XX

PN EP370453-A.

XX

PD 30-MAY-1990.

XX

PF 21-NOV-1989; 89EP-00121498.

XX

PR 19-MAY-1989; 89DE-03916291.

PR 03-JUN-1989; 89DE-03918225.

XX
PA (FARH) HOECHST AG.
XX
PI Henke S, Anagnostop H, Breipohl G, Knolle J, Stechel J;
PI Scholken B, Fehihaber HW;
XX
DR WPI; 1990-165194/22.
XX
PT New oligopeptide with tetra:hydro:isoquinoline-carboxylic acid residue -
PT antagonists of bradykinin, for treating e.g. wounds, asthma, allergy,
PT hypotension, etc.
XX
PS Example 40; Page 16; 34pp; German.
XX
CC The peptide is a bradykinin antagonist, so is useful for treating any
CC condition where bradykinin or its analogues are involved, e.g. wounds,
CC burns, erythema, oedema, angina, asthma, allergy, inflammation,
CC hypotension, etc. Compsns. for topical application or inhalation contain
CC 0.01-5 mg/ml and the systemic dose is 0.01-10 mg/ml. (Updated on 25-MAR-
CC 2003 to correct PI field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 1 RRP 3

RESULT 35
AAR09485
ID AAR09485 standard; peptide; 11 AA.
XX
AC AAR09485;
XX
DT 25-MAR-2003 (revised)
DT 17-JUN-1993 (first entry)
XX
DE Bradykinin antagonist having D-Tic (36).
XX
KW 1,2,3,4-tetrahydroisoquinoline-3-ylcarbonyl; wound; burns; erythema;
KW oedema; angina; asthma; allergy; inflammation; hypotension.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "D-form residue"
FT Modified-site 3
FT /note= "hydroxyproline"
FT Modified-site 6
FT /label= OTHER
FT /note= "2-thienylalanyl"
FT Modified-site 9

FT /label= OTHER
FT /note= "D-tetrahydroisoquinoline-3-ylcarbonyl"
XX
PN EP370453-A.
XX
PD 30-MAY-1990.
XX
PF 21-NOV-1989; 89EP-00121498.
XX
PR 19-MAY-1989; 89DE-03916291.
PR 03-JUN-1989; 89DE-03918225.
XX
PA (FARH) HOECHST AG.
XX
PI Henke S, Anagnostop H, Breipohl G, Knolle J, Stechel J;
PI Scholkens B, Fehihaber HW;
XX
DR WPI; 1990-165194/22.
XX
PT New oligopeptide with tetra:hydro:isoquinoline-carboxylic acid residue -
PT antagonists of bradykinin, for treating e.g. wounds, asthma, allergy,
PT hypotension, etc.
XX
PS Example 36; Page 16; 34pp; German.
XX
CC The peptide is a bradykinin antagonist, so is useful for treating any
CC condition where bradykinin or its analogues are involved, e.g. wounds,
CC burns, erythema, oedema, angina, asthma, allergy, inflammation,
CC hypotension, etc. Compsns. for topical application or inhalation contain
CC 0.01-5 mg/ml and the systemic dose is 0.01-10 mg/ml. (Updated on 25-MAR-
CC 2003 to correct PI field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 1 RRP 3

RESULT 36
AAR09463
ID AAR09463 standard; peptide; 11 AA.
XX
AC AAR09463;
XX
DT 25-MAR-2003 (revised)
DT 17-JUN-1993 (first entry)
XX
DE Bradykinin antagonist having D-Tic (14).
XX
KW 1,2,3,4-tetrahydroisoquinoline-3-ylcarbonyl; wound; burns; erythema;
KW oedema; angina; asthma; allergy; inflammation; hypotension.
XX

OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "D-form residue"
FT Modified-site 3
FT /note= "hydroxyproline"
FT Modified-site 6
FT /label= OTHER
FT /note= "2-thienylalanyl"
FT Modified-site 8
FT /label= OTHER
FT /note= "D-tetrahydroisoquinoline-3-ylcarbonyl"
XX
PN EP370453-A.
XX
PD 30-MAY-1990.
XX
PF 21-NOV-1989; 89EP-00121498.
XX
PR 19-MAY-1989; 89DE-03916291.
PR 03-JUN-1989; 89DE-03918225.
XX
PA (FARH) HOECHST AG.
XX
PI Henke S, Anagnostop H, Breipohl G, Knolle J, Stechel J;
PI Scholvens B, Fehihaber HW;
XX
DR WPI; 1990-165194/22.
XX
PT New oligopeptide with tetra:hydro:isoquinoline-carboxylic acid residue -
PT antagonists of bradykinin, for treating e.g. wounds, asthma, allergy,
PT hypotension, etc.
XX
PS Example 14; Page 13; 34pp; German.
XX
CC The peptide is a bradykinin antagonist, so is useful for treating any
CC condition where bradykinin or its analogues are involved, e.g. wounds,
CC burns, erythema, oedema, angina, asthma, allergy, inflammation,
CC hypotension, etc. Compsns. for topical application or inhalation contain
CC 0.01-5 mg/ml and the systemic dose is 0.01-10 mg/ml. (Updated on 25-MAR-
CC 2003 to correct PI field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 1 RRP 3

RESULT 37
AAR09488
ID AAR09488 standard; peptide; 11 AA.

XX
AC AAR09488;
XX
DT 25-MAR-2003 (revised)
DT 17-JUN-1993 (first entry)
XX
DE Bradykinin antagonist having D-Tic (39).
XX
KW 1,2,3,4-tetrahydroisoquinoline-3-ylcarbonyl; wound; burns; erythema;
KW oedema; angina; asthma; allergy; inflammation; hypotension.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "D-form residue"
FT Modified-site 3
FT /note= "hydroxyproline"
FT Modified-site 6
FT /label= OTHER
FT /note= "2-thienylalanyl"
FT Modified-site 8
FT /label= bALA
FT Modified-site 9
FT /label= OTHER
FT /note= "D-tetrahydroisoquinoline-3-ylcarbonyl"
FT Modified-site 10
FT /label= OTHER
FT /note= "cis,endo-2-azabicyclo[3.3.0]octane -3-S-carbonyl"
XX
PN EP370453-A.
XX
PD 30-MAY-1990.
XX
PF 21-NOV-1989; 89EP-00121498.
XX
PR 19-MAY-1989; 89DE-03916291.
PR 03-JUN-1989; 89DE-03918225.
XX
PA (FARH) HOECHST AG.
XX
PI Henke S, Anagnostop H, Breipohl G, Knolle J, Stechel J;
PI Scholkens B, Fehihaber HW;
XX
DR WPI; 1990-165194/22.
XX
PT New oligopeptide with tetra:hydro:isoquinoline-carboxylic acid residue -
PT antagonists of bradykinin, for treating e.g. wounds, asthma, allergy,
PT hypotension, etc.
XX
PS Example 39; Page 16; 34pp; German.
XX
CC The peptide is a bradykinin antagonist, so is useful for treating any
CC condition where bradykinin or its analogues are involved, e.g. wounds,
CC burns, erythema, oedema, angina, asthma, allergy, inflammation,
CC hypotension, etc. Compsns. for topical application or inhalation contain
CC 0.01-5 mg/ml and the systemic dose is 0.01-10 mg/ml. (Updated on 25-MAR-

CC 2003 to correct PI field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 1 RRP 3

RESULT 38

AAR09491

ID AAR09491 standard; peptide; 11 AA.

XX

AC AAR09491;

XX

DT 25-MAR-2003 (revised)

DT 17-JUN-1993 (first entry)

XX

DE Bradykinin antagonist having D-Tic (42).

XX

KW 1,2,3,4-tetrahydroisoquinoline-3-ylcarbonyl; wound; burns; erythema;

KW oedema; angina; asthma; allergy; inflammation; hypotension.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1

FT /note= "D-form residue"

FT Modified-site 4

FT /note= "hydroxyproline"

FT Modified-site 6

FT /label= OTHER

FT /note= "2-thienylalanyl"

FT Modified-site 8

FT /label= OTHER

FT /note= "D-tetrahydroisoquinoline-3-ylcarbonyl"

XX

PN EP370453-A.

XX

PD 30-MAY-1990.

XX

PF 21-NOV-1989; 89EP-00121498.

XX

PR 19-MAY-1989; 89DE-03916291.

PR 03-JUN-1989; 89DE-03918225.

XX

PA (FARH) HOECHST AG.

XX

PI Henke S, Anagnostop H, Breipohl G, Knolle J, Stechel J;

PI Scholkens B, Fehihaber HW;

XX

DR WPI; 1990-165194/22.

XX

PT New oligopeptide with tetra:hydro:isoquinoline-carboxylic acid residue -
PT antagonists of bradykinin, for treating e.g. wounds, asthma, allergy,
PT hypotension, etc.

XX

PS Example 42; Page 16; 34pp; German.

XX

CC The peptide is a bradykinin antagonist, so is useful for treating any
CC condition where bradykinin or its analogues are involved, e.g. wounds,
CC burns, erythema, oedema, angina, asthma, allergy, inflammation,
CC hypotension, etc. Compsns. for topical application or inhalation contain
CC 0.01-5 mg/ml and the systemic dose is 0.01-10 mg/ml. (Updated on 25-MAR-
CC 2003 to correct PI field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 1 RRP 3

RESULT 39

AAR09486

ID AAR09486 standard; peptide; 11 AA.

XX

AC AAR09486;

XX

DT 25-MAR-2003 (revised)

DT 17-JUN-1993 (first entry)

XX

DE Bradykinin antagonist having D-Tic (37).

XX

KW 1,2,3,4-tetrahydroisoquinoline-3-ylcarbonyl; wound; burns; erythema;

KW oedema; angina; asthma; allergy; inflammation; hypotension.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1

FT /note= "D-form residue"

FT Modified-site 4

FT /note= "hydroxyproline"

FT Modified-site 6

FT /label= OTHER

FT /note= "2-thienylalanyl"

FT Modified-site 9

FT /label= OTHER

FT /note= "D-tetrahydroisoquinoline-3-ylcarbonyl"

XX

PN EP370453-A.

XX

PD 30-MAY-1990.

XX

PF 21-NOV-1989; 89EP-00121498.

XX
PR 19-MAY-1989; 89DE-03916291.
PR 03-JUN-1989; 89DE-03918225.
XX
PA (FARH) HOECHST AG.
XX
PI Henke S, Anagnostop H, Breipohl G, Knolle J, Stechel J;
PI Scholkens B, Fehihaber HW;
XX
DR WPI; 1990-165194/22.
XX
PT New oligopeptide with tetra:hydro:isoquinoline-carboxylic acid residue -
PT antagonists of bradykinin, for treating e.g. wounds, asthma, allergy,
PT hypotension, etc.
XX
PS Example 37; Page 16; 34pp; German.
XX
CC The peptide is a bradykinin antagonist, so is useful for treating any
CC condition where bradykinin or its analogues are involved, e.g. wounds,
CC burns, erythema, oedema, angina, asthma, allergy, inflammation,
CC hypotension, etc. Compsns. for topical application or inhalation contain
CC 0.01-5 mg/ml and the systemic dose is 0.01-10 mg/ml. (Updated on 25-MAR-
CC 2003 to correct PI field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 1 RRP 3

RESULT 40
AAR09461
ID AAR09461 standard; peptide; 11 AA.
XX
AC AAR09461;
XX
DT 25-MAR-2003 (revised)
DT 17-JUN-1993 (first entry)
XX
DE Bradykinin antagonist having D-Tic (12).
XX
KW 1,2,3,4-tetrahydroisoquinoline-3-ylcarbonyl; wound; burns; erythema;
KW oedema; angina; asthma; allergy; inflammation; hypotension.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "D-form residue"
FT Modified-site 3
FT /note= "hydroxyproline"
FT Modified-site 6

FT /label= OTHER
 FT /note= "2-thienylalanyl"
 FT Modified-site 9
 FT /label= OTHER
 FT /note= "D-tetrahydroisoquinoline-3-ylcarbonyl"
 XX
 PN EP370453-A.
 XX
 PD 30-MAY-1990.
 XX
 PF 21-NOV-1989; 89EP-00121498.
 XX
 PR 19-MAY-1989; 89DE-03916291.
 PR 03-JUN-1989; 89DE-03918225.
 XX
 PA (FARH) HOECHST AG.
 XX
 PI Henke S, Anagnostop H, Breipohl G, Knolle J, Stechel J;
 PI Scholvens B, Fehihaber HW;
 XX
 DR WPI; 1990-165194/22.
 XX
 PT New oligopeptide with tetra:hydro:isoquinoline-carboxylic acid residue -
 PT antagonists of bradykinin, for treating e.g. wounds, asthma, allergy,
 PT hypotension, etc.
 XX
 PS Example 12; Page 13; 34pp; German.
 XX
 CC The peptide is a bradykinin antagonist, so is useful for treating any
 CC condition where bradykinin or its analogues are involved, e.g. wounds,
 CC burns, erythema, oedema, angina, asthma, allergy, inflammation,
 CC hypotension, etc. Compsns. for topical application or inhalation contain
 CC 0.01-5 mg/ml and the systemic dose is 0.01-10 mg/ml. (Updated on 25-MAR-
 CC 2003 to correct PI field.)
 XX
 SQ Sequence 11 AA;

 Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 8 RRP 10
 |||
 Db 1 RRP 3

RESULT 41
 AAR09464
 ID AAR09464 standard; peptide; 11 AA.
 XX
 AC AAR09464;
 XX
 DT 25-MAR-2003 (revised)
 DT 17-JUN-1993 (first entry)
 XX
 DE Bradykinin antagonist having D-Tic (15).
 XX

KW 1,2,3,4-tetrahydroisoquinoline-3-ylcarbonyl; wound; burns; erythema;
KW oedema; angina; asthma; allergy; inflammation; hypotension.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "D-form residue"
FT Modified-site 3
FT /note= "hydroxyproline"
FT Modified-site 6
FT /label= OTHER
FT /note= "2-thienylalanyl"
FT Modified-site 8
FT /label= bALA
FT Modified-site 9
FT /label= OTHER
FT /note= "D-tetrahydroisoquinoline-3-ylcarbonyl"

XX

PN EP370453-A.

XX

PD 30-MAY-1990.

XX

PF 21-NOV-1989; 89EP-00121498.

XX

PR 19-MAY-1989; 89DE-03916291.

PR 03-JUN-1989; 89DE-03918225.

XX

PA (FARH) HOECHST AG.

XX

PI Henke S, Anagnostop H, Breipohl G, Knolle J, Stechel J;
PI Scholkens B, Fehihaber HW;

XX

DR WPI; 1990-165194/22.

XX

PT New oligopeptide with tetra:hydro:isoquinoline-carboxylic acid residue -
PT antagonists of bradykinin, for treating e.g. wounds, asthma, allergy,
PT hypotension, etc.

XX

PS Example 15; Page 13; 34pp; German.

XX

CC The peptide is a bradykinin antagonist, so is useful for treating any
CC condition where bradykinin or its analogues are involved, e.g. wounds,
CC burns, erythema, oedema, angina, asthma, allergy, inflammation,
CC hypotension, etc. Compsns. for topical application or inhalation contain
CC 0.01-5 mg/ml and the systemic dose is 0.01-10 mg/ml. (Updated on 25-MAR-
CC 2003 to correct PI field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||

Db 1 RRP 3

RESULT 42
AAR03387
ID AAR03387 standard; protein; 11 AA.
XX
AC AAR03387;
XX
DT 25-MAR-2003 (revised)
DT 31-JUL-1990 (first entry)
XX
DE Fragment of pertussis toxin S1 subunit.
XX
KW Whooping cough; subunit S1; vaccine.
XX
OS *Bordetella pertussis*.
XX
PN WO9001494-A.
XX
PD 22-FEB-1990.
XX
PF 31-JUL-1989; 89WO-US003298.
XX
PR 02-AUG-1988; 88US-00227372.
XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX
PI Steinman L, Oksenbergs JR, Schoolnik GK, Judd AK;
XX
DR WPI; 1990-083476/11.
XX
PT Polypeptide(s) useful as *Bordetella pertussis* vaccines - comprise
PT specified sequence(s) of S1 subunit.
XX
PS Disclosure; Page ?; 41pp; English.
XX
CC Useful as a vaccine for whooping cough, free from the side effects
CC associated with the intact S1 subunit. (Updated on 25-MAR-2003 to correct
CC PF field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-
CC MAR-2003 to correct DR field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TGR 8
|||
Db 8 TGR 10

RESULT 43
AAR05912
ID AAR05912 standard; protein; 11 AA.
XX
AC AAR05912;

XX
DT 31-OCT-2002 (revised)
DT 26-NOV-1990 (first entry)
XX
DE Partial sequence of GAP-43 associated protein p34-A.
XX
KW Internal regulatory protein; IRP; neuronal growth related peptide;
KW GAP-43; membrane targetting peptide; MTP; ischaemia; hypoxia; stroke.
XX
OS Homo sapiens.
XX
PN WO9006948-A.
XX
PD 28-JUN-1990.
XX
PF 22-DEC-1988; 88US-00288604.
XX
PR 22-DEC-1988; 88US-00288604.
PR 02-FEB-1989; 89US-00305239.
PR 01-SEP-1989; 89US-00401408.
XX
PA (FISH/) FISHMAN M C.
XX
PI Fishman MC, Zuber MX, Strittmat SM, Valenzuela D;
XX
DR WPI; 1990-224493/29.
XX
PT Mammalian neuronal growth peptide GAP-43 and corresp. DNA - also new
PT membrane targetting and internal regulatory peptide(s), useful e.g. for
PT neuronal modelling and healing neural tissue damage.
XX
PS Example 8; Fig 16; 9pp; English.
XX
CC GAP-43 is useful in structural remodelling of neural cells and treatment
CC of ischaemia, hypoxia, stroke and other neural tissue damage. (Updated on
CC 31-OCT-2002 to add missing OS field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TNK 4
|||
Db 9 TNK 11

RESULT 44
AAR08092
ID AAR08092 standard; protein; 11 AA.
XX
AC AAR08092;
XX
DT 25-MAR-2003 (revised)
DT 01-MAR-1991 (first entry)
XX

DE Antifreeze segment #2 encoded by SS3.
XX
KW synthetic antifreeze polypeptide; cryopreservation;
KW core repetitive sequence.
XX
OS Synthetic.
XX
PN WO9013571-A.
XX
PD 15-NOV-1990.
XX
PF 10-MAY-1989; 89US-00350481.
XX
PR 10-MAY-1989; 89US-00350481.
PR 10-APR-1990; 90US-00507716.
XX
PA (DNAP) DNA PLANT TECHN COR.
XX
PI Warren GJ, Mueller JM, Mckown RJ, Dunsmuir P;
XX
DR WPI; 1990-361428/48.
XX
PT New anti-freeze poly-peptide(s) - used for cryo-protection of e.g. foods,
PT medically used biological(s), plant prods. or plants during growth.
XX
PS Disclosure; Fig 4; 111pp; English.
XX
CC Synthetic anti-freeze polypeptides (saf) comprise a specifically
CC cleavable site and a region containing at least two "core" segments such
CC as the 11mer given here. The saf's suppress ice crystal growth by binding
CC to the growing crystal face and blocking sites for further crystal
CC growth. They can be used to maximise retention of important properties of
CC organic materials through freezing and thawing processes. The basic
CC design of the polypeptides is based on known antifreeze polypeptides from
CC insects and fish, e.g. the winter flounder. See also AAQ06649-Q06652,
CC AAQ06656, AAQ06658, AAQ06660-Q06672, AAR08070-6, AAR08087-R08091,
CC AAR08093. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-
CC MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI
CC field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 KKT 6
|||
Db 9 KKT 11

RESULT 45
AAR28593
ID AAR28593 standard; protein; 11 AA.
XX
AC AAR28593;
XX

DT 25-MAR-2003 (revised)
DT 03-APR-1993 (first entry)
XX
DE Partial sequence of growth cone membrane fraction p-34-A which is
DE identical to beta 1 79-89 and beta 2 79-89.
XX
KW Neuronal growth-related protein; axon; GAP-43 protein.
XX
OS Rattus rattus.
XX
PN WO9218138-A1.
XX
PD 29-OCT-1992.
XX
PF 10-APR-1992; 92WO-US003014.
XX
PR 10-APR-1991; 91US-00683455.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Fishman MC, Federoff HJ, Zuber MX, Strittmatter SM, Valenzuela D;
XX
DR WPI; 1992-381769/46.
XX
PT Recombinant mammalian GAP-43 - used in the study, diagnosis and treatment
PT of damaged, diseased or dysfunctional nervous system tissue.
XX
PS Example; Fig 16; 191pp; English.
XX
CC A growth cone membrane fraction was prep'd. from neonatal rat brain.
CC Prominent proteins with Mrs of about 35,000 and 40,000 have been termed
CC p34 and p38, and are specifically enriched in the growth cone membrane.
CC It was noted that p34 and p38 have similar mol. wts. to the alpha and
CC beta subunits of the GTP-binding protein G0. Co-electrophoresis of the
CC growth cone membranes with purified bovine grain G0 demonstrated that p34
CC co-migrates with the beta subunit, and p38 with the alpha subunit of G0.
CC Partial protein sequences were obtained from electrophoretically purified
CC p34 and p38. The sequence for each of three peptides from p38 was
CC identical to that of alpha0. The three p34 peptides had a sequence
CC identical to that of the beta subunit of G proteins. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TNK 4
|||
Db 9 TNK 11

RESULT 46
AAR25458
ID AAR25458 standard; protein; 11 AA.
XX

AC AAR25458;
XX
DT 25-MAR-2003 (revised)
DT 15-JAN-1993 (first entry)
XX
DE wohl-5.
XX
KW PF4; Behcet's disease; angiogenic response.
XX
OS Synthetic.
XX
PN WO9211021-A1.
XX
PD 09-JUL-1992.
XX
PF 20-DEC-1991; 91WO-US009813.
XX
PR 21-DEC-1990; 90US-00631823.
XX
PA (CURA-) CURATIVE TECHNOLOGIES INC.
XX
PI Whitman RB, Wohl R, Duff RG;
XX
DR WPI; 1992-249845/30.
XX
PT New angiogenic peptide(s) derived from platelet factor 4 - used to
PT promote wound healing in patients with vascular insufficiency, diabetes,
PT pressure ulcers etc.
XX
PS Claim 10; Page 23; 39pp; English.
XX
CC The sequences given in AAR25454-61 angiogenic peptides which are derived
CC from platelet faactor 4 (PF4). PF4 is a 70 amino acid heparin-binding
CC protein and is released from the alpha granules of activated platelets.
CC Increased levels of PF4 have been found in diabetic patients and in
CC patients with Behcet's disease. The peptide sequences given are capable
CC of inducing an angiogenic response in vivo. These peptides may be
CC particularly useful in promoting wound healing, including incisional
CC healing, bone repair, burn healing, and post-infarction repair in
CC myocardial or central nervous system injury; and the assimilation of
CC grafted tissues, particularly in persons suffering from vascular
CC insufficiency, such as diabetic patients. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 6 RPR 8

RESULT 47
AAR26211

ID AAR26211 standard; peptide; 11 AA.
XX
AC AAR26211;
XX
DT 25-MAR-2003 (revised)
DT 28-JAN-1993 (first entry)
XX
DE Sequence of angiogenic peptide derived from platelet factor 4 (PF4).
XX
KW Angiogenic peptide; wound healing; platelet factor 4; vascularisation.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 6. .9
FT /note= "claimed fragment"
XX
PN WO9213874-A2.
XX
PD 20-AUG-1992.
XX
PF 02-JAN-1992; 92WO-US000099.
XX
PR 02-JAN-1991; 91US-00636798.
XX
PA (FOXC-) FOX CHASE CANCER CENT.
XX
PI Mintz B;
XX
DR WPI; 1992-299977/36.
XX
PT New peptide(s) derived from platelet factor 4 - have angiogenic activity,
PT useful in treating vascular insufficiency, diabetes and for wound
PT healing.
XX
PS Claim 10; Page 19; 22pp; English.
XX
CC An octapeptide derived from platelet factor 4 and seven structurally
CC related peptides (see AAR26210-12) are capable of inducing an angiogenic
CC response in vivo as measured by neovascularization in rabbit corneal
CC implant assay and by measurement of capillary endothelial cell
CC chemoattraction. The angiogenic peptides may be particularly useful in
CC promoting wound healing, and the assimilation of grafted tissues.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 RPR 11
|||
Db 6 RPR 8

AAR37243

ID AAR37243 standard; peptide; 11 AA.

XX

AC AAR37243;

XX

DT 10-MAR-2003 (revised)

DT 06-SEP-1993 (first entry)

XX

DE IL-6 antagonist peptide #27.

XX

KW IL-6; antagonist; cytokine; B cell differentiation; inflammation;

KW tissue injury; B9.9 hybridoma cell line; Castleman's Disease;

KW Lennart's T-cell lymphoma; Non-Hodgkin's lymphoma; allergy;

KW immune deficiency disease; cardiac myxoma;

KW mesangial proliferative glomerulonephritis.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN US5210075-A.

XX

PD 11-MAY-1993.

XX

PF 16-FEB-1990; 90US-00480868.

XX

PR 16-FEB-1990; 90US-00480868.

XX

PA (TANA) TANABE SEIYAKU CO.

XX

PI Scholz W, Chiang S, Nagarajan G, Lobl TJ;

XX

DR WPI; 1993-166970/20.

XX

PT New peptide interleukin-6 antagonists - for treating and preventing auto-immune, immuno:inflammatory, neoplastic and infectious diseases etc.

XX

PS Example 3; Col 27; 20pp; English.

XX

CC This peptide is a specific example of a highly generic claimed formula
CC covering sequences derived from the p51-70 portion (i.e the IL-6 receptor
CC -binding portion) of IL-6 (see AAR37216) or modelled after different
CC portions of this sequence. In an assay to determine IL-6 antagonist
CC activity of this peptide, proliferation of the IL-6 dependent B9.9
CC hybridoma cell line (J.Immunol. 139: 4116, 1987) was inhibited by 91 (+/-
CC 2)%. See AAR37216-R37261. (Updated on 10-MAR-2003 to add missing OS
CC field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9

|||

Db 9 GRR 11

RESULT 49
AAR44847
ID AAR44847 standard; peptide; 11 AA.
XX
AC AAR44847;
XX
DT 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 31-JAN-1994 (first entry)
XX
DE Lactoferrin-related antibacterial peptide.
XX
KW Lactoferrin; antibiotic; chelate; mastitis; bowel disorder; disease;
KW bacteria; yeast; fungi; disinfection; drug; foodstuff; cosmetic;
KW toiletries.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 10
FT /note= "Cys10 forms disulfide bond with Cys35 of sequence
FT in AAR44846"
XX
PN WO9314640-A1.
XX
PD 05-AUG-1993.
XX
PF 30-NOV-1992; 92WO-JP001563.
XX
PR 23-JAN-1992; 92JP-00032660.
PR 11-MAR-1992; 92JP-00052943.
PR 30-SEP-1992; 92JP-00262143.
PR 30-SEP-1992; 92JP-00262559.
XX
PA (MORG) MORINAGA MILK IND CO LTD.
XX
PI Tomita M, Shimamura S, Kawase K, Fukuwatari Y, Takase M;
PI Bellamy W, Yamauchi K, Wakabayashi H, Tokita Y;
XX
DR WPI; 1993-258265/32.
XX
PT Antibacterial agent comprising decomposition products of lactoferrin -
PT with chelate e.g. EDTA alcohol and/or antibiotic e.g. penicillin, also
PT useful against yeast and fungi.
XX
PS Disclosure; Page 88; 100pp; Japanese.
XX
CC Lactoferrin-related peptides are used in new antibacterial compsn. The
CC compsn. is highly effective against a broad range of bacteria, yeasts and
CC fungi. It can be used therapeutically (internal and external
CC application), e.g. for mastitis, bowel disorders, urinary infections,
CC etc. It can also be used for the disinfection and protection of drugs,
CC foodstuffs, cosmetics and toiletries and household items (such as kitchen
CC towels and toilet paper). (Updated on 09-JAN-2003 to add missing OS
CC field.) (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
|||
Db 1 GRR 3

RESULT 50

AAR38680

ID AAR38680 standard; peptide; 11 AA.

XX

AC AAR38680;

XX

DT 25-MAR-2003 (revised)

DT 01-NOV-1993 (first entry)

XX

DE Bradykinin antagonist (4).

XX

KW Oedema; pancreas; enzyme; acute pancreatitis; serum amylase; lipase;

KW hypovolaemia; hyperalbuminaemia; pain.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "(4-benzoyl)benzoyl-Lys"

FT Misc-difference 2

FT /note= "D-form residue"

FT Modified-site 5

FT /note= "hydroxyproline"

FT Modified-site 7

FT /note= "2-thienylalanine"

FT Modified-site 9

FT /note= "D-1,2,3,4 tetrahydroisoquinoline-3-yl-carbonyl"

FT Modified-site 10

FT /note= "cis, endo octahydroindolecarbonyl"

XX

PN EP548825-A1.

XX

PD 30-JUN-1993.

XX

PF 18-DEC-1992; 92EP-00121558.

XX

PR 21-DEC-1991; 91EP-00122055.

XX

PA (FARH) HOECHST AG.

XX

PI Griesbacher T, Lembeck F;

XX

DR WPI; 1993-206998/26.

XX

PT Compsn. to treat acute pancreatitis - comprising peptide(s) as bradykinin antagonists.

XX
PS Claim 4; Page 11; 16pp; English.
XX
CC This sequence is an example of a highly generic formula. The peptide is a
CC bradykinin antagonist which prevents bradykinin-induced oedema and thus
CC allows pancreatic enzymes to leave the tissue without hindrance. The
CC peptide is useful in the treatment of acute pancreatitis which is
CC characterised by a massive oedema of the gland and the retroperitoneal
CC tissue, interstitial activation of proteolytic enzymes, elevation of
CC serum amylase and lipase levels, hypovolaemia, hyperalbuminaemia,
CC pulmonary oedema and severe pain. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 2 RRP 4

RESULT 51
AAR33285
ID AAR33285 standard; protein; 11 AA.
XX
AC AAR33285;
XX
DT 25-MAR-2003 (revised)
DT 13-MAY-1993 (first entry)
XX
DE pDS56/RBSII(-2) produced peptide.
XX
KW Plasmid; pDS56/RBSII; -1; -2; regulatable; promoter; operator;
KW N25OPSN25OP29; ribosomal binding site; RBS; RBSII; RBSII(-1); RBSII(-2);
KW Pg25; E. coli; phage; T5; lac; repressor; lacI; lacIq; pDMI.1;
KW replication; beta-lactamase; terminator; lambda; CAT; T1;
KW chloramphenicol acetyltransferase; rrnB operon; reading frame.
XX
OS Synthetic.
XX
PN EP522482-A2.
XX
PD 13-JAN-1993.
XX
PF 06-JUL-1992; 92EP-00111407.
XX
PR 12-JUL-1991; 91US-00729099.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Binger M, Pasamontes L;
XX
DR WPI; 1993-010336/02.
DR N-PSDB; AAQ34609.

XX
PT Immunogenic specified polypeptide and fragments - capable of inducing an
PT immune response against eimeria parasites and free from proteins produced
PT by these parasites.
XX
PS Disclosure; Fig 8; 72pp; English.
XX
CC The sequences given in AAR33283-85 represent the peptides which are
CC encoded by the open reading frames under the control of the ribosome
CC binding sites (RBS) in plasmids pDS56/RBSII, -1, and -2 . These plasmids
CC contain the regulatable promoter/operator element N250PSN250P29 and the
CC RBS's RBSII, RBSII(-1) and RBSII(-2) respectively. These RBS are derived
CC from the RBS of the promoter Pg25 of the E. coli phage T5. These plasmids
CC may be maintained in E. coli only if the promoter/operator element is
CC repressed by the binding of a lac repressor to the operator. The lac
CC repressor is encoded by the lacI gene. N250PSN250P29 can be repressed
CC efficiently only when a sufficient amount of repressor molecules are
CC present in the cells. Therefore the lacIq allele, which contains a
CC promoter mutant responsible for increased expression of the repressor
CC gene was used. This lacIq allele is present on the plasmid pDMI.1
CC (AAQ34610). The region of these plasmids between bases 1-1120 contains
CC the replication region and the gene for beta-lactamase. The beta-
CC lactamase gene is modified by elimination of the HincIII and PstI
CC cleavage sites. These plasmids also contain cleavage sites for the
CC enzymes SalI, PstI and HindIII, the terminator of E. coli phage lambda,
CC the promoter-free gene of chloramphenicol acetyltransferase (CAT) and the
CC terminator T1 of the E. coli rrnB operon. These plasmids differ by one
CC nucleotide following the ATG start codon resulting in protein expressio
CC in all three potential reading frames. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 4 RRP 6

RESULT 52
AAR40874
ID AAR40874 standard; protein; 11 AA.
XX
AC AAR40874;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 28-MAR-1994 (first entry)
XX
DE SSP for flavonoid-3',5'-hydroxylase gene.
XX
KW Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;
KW tobacco; pigment alteration; blue; SSP; single specific primer; PCR;
KW polymerase chain reaction; amplification; expression; ss.

XX
OS Petunia x hybrida.
XX
PN WO9318155-A1.
XX
PD 16-SEP-1993.
XX
PF 20-NOV-1992; 92WO-JP001520.
XX
PR 02-MAR-1992; 92JP-00044963.
XX
PA (KYOW) KYOWA HAKKO KOGYO CO LTD.
XX
PI Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;
PI Okinaka Y;
XX
DR WPI; 1993-303469/38.
DR N-PSDB; AAQ47875.
XX
PT Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to
PT transform plants e.g. petunia, rose or tobacco to give bluer flower
PT colour and altered pigment pattern.
XX
PS Claim 11; Page 57; 82pp; Japanese.
XX
CC Insertion of the sequences (AAQ47840-42) into plants such as rose,
CC petunia, tobacco and carnation, using a suitable vector such as
CC agrobacterium, give transformed plants which express the gene, resulting
CC in petals with a bluer colour than normal, and/or pigmentation patterns
CC which do not occur naturally. The sequences were amplified using primers
CC (AAQ47843-70). Related single specific primers using a gene sequence
CC coding for the haem-binding region of cytochrome P450 are shown in
CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
|||
Db 5 GRR 7

RESULT 53
AAR40872
ID AAR40872 standard; protein; 11 AA.
XX
AC AAR40872;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 28-MAR-1994 (first entry)
XX
DE SSP for flavonoid-3',5'-hydroxylase gene product.

XX
KW Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;
KW tobacco; pigment alteration; blue; SSP; single specific primer; PCR;
KW polymerase chain reaction; amplification; expression.
XX
OS Petunia x hybrida.
XX
PN WO9318155-A1.
XX
PD 16-SEP-1993.
XX
PF 20-NOV-1992; 92WO-JP001520.
XX
PR 02-MAR-1992; 92JP-00044963.
XX
PA (KYOW) KYOWA HAKKO KOGYO CO LTD.
XX
PI Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;
PI Okinaka Y;
XX
DR WPI; 1993-303469/38.
DR N-PSDB; AAQ47873.
XX
PT Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to
PT transform plants e.g. petunia, rose or tobacco to give bluer flower
PT colour and altered pigment pattern.
XX
PS Claim 11; Page 56; 82pp; Japanese.
XX
CC Insertion of the sequences (AAQ47840-42) into plants such as rose,
CC petunia, tobacco and carnation, using a suitable vector such as
CC agrobacterium, give transformed plants which express the gene, resulting
CC in petals with a bluer colour than normal, and/or pigmentation patterns
CC which do not occur naturally. The sequences were amplified using primers
CC (AAQ47843-70). Related single specific primers using a gene sequence
CC coding for the haem-binding region of cytochrome P450 are shown in
CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GRR 9
|||
Db 5 GRR 7

RESULT 54
AAR41634
ID AAR41634 standard; protein; 11 AA.
XX
AC AAR41634;
XX
DT 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)
DT 28-MAR-1994 (first entry)
XX
DE SSP for flavonoid-3',5'-hydroxylase gene product.
XX
KW Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;
KW tobacco; pigment alteration; blue; SSP; single specific primer; PCR;
KW polymerase chain reaction; amplification; expression.
XX
OS Petunia x hybrida.
XX
PN WO9318155-A1.
XX
PD 16-SEP-1993.
XX
PF 20-NOV-1992; 92WO-JP001520.
XX
PR 02-MAR-1992; 92JP-00044963.
XX
PA (KYOW) KYOWA HAKKO KOGYO CO LTD.
XX
PI Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;
PI Okinaka Y;
XX
DR WPI; 1993-303469/38.
DR N-PSDB; AAQ47883.
XX
PT Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to
PT transform plants e.g. petunia, rose or tobacco to give bluer flower
PT colour and altered pigment pattern.
XX
PS Claim 11; Page 61; 82pp; Japanese.
XX
CC Insertion of the sequences (AAQ47840-42) into plants such as rose,
CC petunia, tobacco and carnation, using a suitable vector such as
CC agrobacterium, give transformed plants which express the gene, resulting
CC in petals with a bluer colour than normal, and/or pigmentation patterns
CC which do not occur naturally. The sequences were amplified using primers
CC (AAQ47843-70). Related single specific primers using a gene sequence
CC coding for the haem-binding region of cytochrome P450 are shown in
CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
|||
Db 5 GRR 7

RESULT 55
AAR40878
ID AAR40878 standard; protein; 11 AA.

XX
AC AAR40878;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 28-MAR-1994 (first entry)
XX
DE SSP for flavonoid-3',5'-hydroxylase gene product.
XX
KW Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;
KW tobacco; pigment alteration; blue; SSP; single specific primer; PCR;
KW polymerase chain reaction; amplification; expression.
XX
OS Petunia x hybrida.
XX
PN WO9318155-A1.
XX
PD 16-SEP-1993.
XX
PF 20-NOV-1992; 92WO-JP001520.
XX
PR 02-MAR-1992; 92JP-00044963.
XX
PA (KYOW) KYOWA HAKKO KOGYO CO LTD.
XX
PI Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;
PI Okinaka Y;
XX
DR WPI; 1993-303469/38.
DR N-PSDB; AAQ47879.
XX
PT Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to
PT transform plants e.g. petunia, rose or tobacco to give bluer flower
PT colour and altered pigment pattern.
XX
PS Claim 11; Page 58; 82pp; Japanese.
XX
CC Insertion of the sequences (AAQ47840-42) into plants such as rose,
CC petunia, tobacco and carnation, using a suitable vector such as
CC agrobacterium, give transformed plants which express the gene, resulting
CC in petals with a bluer colour than normal, and/or pigmentation patterns
CC which do not occur naturally. The sequences were amplified using primers
CC (AAQ47843-70). Related single specific primers using a gene sequence
CC coding for the haem-binding region of cytochrome P450 are shown in
CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
|||
Db 5 GRR 7

RESULT 56

AAR40870

ID AAR40870 standard; protein; 11 AA.

XX

AC AAR40870;

XX

DT 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 28-MAR-1994 (first entry)

XX

DE SSP for flavonoid-3',5'-hydroxylase gene product.

XX

KW Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;

KW tobacco; pigment alteration; blue; SSP; single specific primer; PCR;

KW polymerase chain reaction; amplification; expression.

XX

OS Petunia x hybrida.

XX

PN WO9318155-A1.

XX

PD 16-SEP-1993.

XX

PF 20-NOV-1992; 92WO-JP001520.

XX

PR 02-MAR-1992; 92JP-00044963.

XX

PA (KYOW) KYOWA HAKKO KOGYO CO LTD.

XX

PI Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;

PI Okinaka Y;

XX

DR WPI; 1993-303469/38.

DR N-PSDB; AAQ47871.

XX

PT Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to
PT transform plants e.g. petunia, rose or tobacco to give bluer flower
PT colour and altered pigment pattern.

XX

PS Claim 11; Page 55; 82pp; Japanese.

XX

CC Insertion of the sequences (AAQ47840-42) into plants such as rose,
CC petunia, tobacco and carnation, using a suitable vector such as
CC agrobacterium, give transformed plants which express the gene, resulting
CC in petals with a bluer colour than normal, and/or pigmentation patterns
CC which do not occur naturally. The sequences were amplified using primers
CC (AAQ47843-70). Related single specific primers using a gene sequence
CC coding for the haem-binding region of cytochrome P450 are shown in
CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 24-OCT-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
|||
Db 5 GRR 7

RESULT 57
AAR40871
ID AAR40871 standard; protein; 11 AA.
XX
AC AAR40871;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 28-MAR-1994 (first entry)
XX
DE SSP for flavonoid-3',5'-hydroxylase gene product.
XX
KW Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;
KW tobacco; pigment alteration; blue; SSP; single specific primer; PCR;
KW polymerase chain reaction; amplification; expression.
XX
OS Petunia x hybrida.
XX
PN WO9318155-A1.
XX
PD 16-SEP-1993.
XX
PF 20-NOV-1992; 92WO-JP001520.
XX
PR 02-MAR-1992; 92JP-00044963.
XX
PA (KYOW) KYOWA HAKKO KOGYO CO LTD.
XX
PI Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;
PI Okinaka Y;
XX
DR WPI; 1993-303469/38.
DR N-PSDB; AAQ47872.
XX
PT Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to
PT transform plants e.g. petunia, rose or tobacco to give bluer flower
PT colour and altered pigment pattern.
XX
PS Claim 11; Page 55; 82pp; Japanese.
XX
CC Insertion of the sequences (AAQ47840-42) into plants such as rose,
CC petunia, tobacco and carnation, using a suitable vector such as
CC agrobacterium, give transformed plants which express the gene, resulting
CC in petals with a bluer colour than normal, and/or pigmentation patterns
CC which do not occur naturally. The sequences were amplified using primers
CC (AAQ47843-70). Related single specific primers using a gene sequence
CC coding for the haem-binding region of cytochrome P450 are shown in
CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
|||
Db 5 GRR 7

RESULT 58
AAR41635
ID AAR41635 standard; protein; 11 AA.
XX
AC AAR41635;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 28-MAR-1994 (first entry)
XX
DE SSP for flavonoid-3',5'-hydroxylase gene product.
XX
KW Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;
KW tobacco; pigment alteration; blue; SSP; single specific primer; PCR;
KW polymerase chain reaction; amplification; expression.
XX
OS Petunia x hybrida.
XX
PN WO9318155-A1.
XX
PD 16-SEP-1993.
XX
PF 20-NOV-1992; 92WO-JP001520.
XX
PR 02-MAR-1992; 92JP-00044963.
XX
PA (KYOW) KYOWA HAKKO KOGYO CO LTD.
XX
PI Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;
PI Okinaka Y;
XX
DR WPI; 1993-303469/38.
DR N-PSDB; AAQ47885.
XX
PT Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to
PT transform plants e.g. petunia, rose or tobacco to give bluer flower
PT colour and altered pigment pattern.
XX
PS Claim 11; Page 61; 82pp; Japanese.
XX
CC Insertion of the sequences (AAQ47840-42) into plants such as rose,
CC petunia, tobacco and carnation, using a suitable vector such as
CC agrobacterium, give transformed plants which express the gene, resulting
CC in petals with a bluer colour than normal, and/or pigmentation patterns
CC which do not occur naturally. The sequences were amplified using primers
CC (AAQ47843-70). Related single specific primers using a gene sequence
CC coding for the haem-binding region of cytochrome P450 are shown in
CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated

CC on 24-OCT-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
|||
Db 5 GRR 7

RESULT 59

AAR40875

ID AAR40875 standard; protein; 11 AA.

XX

AC AAR40875;

XX

DT 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 28-MAR-1994 (first entry)

XX

DE SSP for flavonoid-3',5'-hydroxylase gene.

XX

KW Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;

KW tobacco; pigment alteration; blue; SSP; single specific primer; PCR;

KW polymerase chain reaction; amplification; expression; ss.

XX

OS Petunia x hybrida.

XX

PN WO9318155-A1.

XX

PD 16-SEP-1993.

XX

PF 20-NOV-1992; 92WO-JP001520.

XX

PR 02-MAR-1992; 92JP-00044963.

XX

PA (KYOW) KYOWA HAKKO KOGYO CO LTD.

XX

PI Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;

PI Okinaka Y;

XX

DR WPI; 1993-303469/38.

DR N-PSDB; AAQ47876.

XX

PT Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to
PT transform plants e.g. petunia, rose or tobacco to give bluer flower
PT colour and altered pigment pattern.

XX

PS Claim 11; Page 57; 82pp; Japanese.

XX

CC Insertion of the sequences (AAQ47840-42) into plants such as rose,
CC petunia, tobacco and carnation, using a suitable vector such as
CC agrobacterium, give transformed plants which express the gene, resulting
CC in petals with a bluer colour than normal, and/or pigmentation patterns

CC which do not occur naturally. The sequences were amplified using primers
CC (AAQ47843-70). Related single specific primers using a gene sequence
CC coding for the haem-binding region of cytochrome P450 are shown in
CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 24-OCT-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

7 GRR 9

|||

Db

5 GRR 7

RESULT 60

AAR31485

ID AAR31485 standard; protein; 11 AA.

XX

AC AAR31485;

XX

DT 25-MAR-2003 (revised)

DT 26-MAY-1993 (first entry)

XX

DE P3 OF 31-34 subunit D band I internal fragment #4.

XX

KW Subunit; D; A; C; B; P3 OF 31-34; osteogenic; active; protein; bone;
KW heterodimer; disulphide bond; formation; repair; defect; human; CNBr;
KW SDS-PAGE.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1

FT /note= "Undetermined amino acid"

FT Misc-difference 5

FT /note= "Undetermined amino acid"

XX

PN WO9300049-A1.

XX

PD 07-JAN-1993.

XX

PF 01-JUL-1991; 91WO-US004686.

XX

PR 20-JUN-1991; 91US-00718274.

XX

PA (XOMA) XOMA CORP.

XX

PI Grinna L, Theofan G, Parsons TF;

XX

DR WPI; 1993-036101/04.

XX

PT Osteogenically active protein preparations for repairing bone defects -
PT comprise hetero-dimer of P3 OF 31-34 sub-unit B and P3 OF 31-34 sub-unit
PT D.

XX
PS Disclosure; Page 27; 107pp; English.
XX
CC The sequences given in AAR31485-90 represent fragments of subunits D, B
CC and A of P3 OF 31-34. These fragments were isolated from bands produced
CC by SDS-PAGE analysis of P3 OF 31-34. Band I was found to contain
CC predominantly subunits B and D, and band II was found to contain
CC predominantly subunits A and C. These bands were subjected to N-terminal
CC sequencing and cleavage with CNBr to generate these fragments. P3 OF 31-
CC 34 is an osteogenically active protein. A primary osteogenically active
CC peptide is formed of a heterodimer of P3 OF 31-34 subunits B and D which
CC are linked by at least one disulphide bond. The B/D heterodimer
CC stimulates osteogenesis and can be used to induce bone formation in
CC mammals, to repair bone defects. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATN 3
|||
Db 2 ATN 4

RESULT 61
AAR54747
ID AAR54747 standard; protein; 11 AA.
XX
AC AAR54747;
XX
DT 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 05-DEC-1994 (first entry)
XX
DE Ad5 fibre DNA fragment.
XX
KW Single chain Fv fragment; ScFv; Gene Therapy; Adenovirus; Primer;
KW Penton fibre; Ad5; Fusion sites; PCR; polymerase chain reaction.
XX
OS unidentified adenovirus.
XX
FH Key Location/Qualifiers
FT Peptide 1..6
FT /label= Ad5 fibre fragment
FT Peptide 7..11
FT /label= ScFv fragment
XX
PN WO9410323-A1.
XX
PD 11-MAY-1994.
XX
PF 04-NOV-1993; 93WO-GB002267.
XX
PR 04-NOV-1992; 92GB-00023084.

XX
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
XX
PI Spooner RA, Epenetos AA;
XX
DR WPI; 1994-167477/20.
DR N-PSDB; AAQ64808.
XX
PT Virus with modified binding moiety specific for the target cells - used
PT to deliver genes for gene therapy and cancer treatment.
XX
PS Example 2; Page 62; 110pp; English.
XX
CC Amplification of Ad5 fibre DNA fragments was carried out by PCR using
CC oligonucleotide AAQ64807 (TAILbBACK) and AAQ64816, or any one of AAQ64808
CC -15. AAR54747 shows a fusion of the Ad5 fibre and ScFv fragment. The
CC invention is concerned with the fusion of an ScFv with the Ad5 fibre such
CC that the fusion sequence can be used to target cells for gene therapy.
CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 KKT 6
|||
Db 3 KKT 5

RESULT 62
AAR54725
ID AAR54725 standard; protein; 11 AA.
XX
AC AAR54725;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 02-DEC-1994 (first entry)
XX
DE ScFv-Ad5 fusion protein C.
XX
KW Single chain Fv fragment; ScFv; Gene Therapy; Adenovirus; Penton fibre;
KW Ad5; Fusion sites.
XX
OS Human adenovirus type 5.
XX
FH Key Location/Qualifiers
FT Peptide 1..6
FT /label= Ad5 fibre
FT Peptide 7..10
FT /label= ScFv fragment
FT Misc-difference 11
FT /label= X represents the remainder of the ScFv fragment.
XX

PN WO9410323-A1.
XX
PD 11-MAY-1994.
XX
PF 04-NOV-1993; 93WO-GB002267.
XX
PR 04-NOV-1992; 92GB-00023084.
XX
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
XX
PI Spooner RA, Epenetos AA;
XX
DR WPI; 1994-167477/20.
DR N-PSDB; AAQ64764.
XX
PT Virus with modified binding moiety specific for the target cells - used
PT to deliver genes for gene therapy and cancer treatment.
XX
PS Example 1; Page 46; 110pp; English.
XX
CC Displaying functional antibody fragments on the surface of recombinant
CC retroviral particles could be used to target replication deficient virus
CC to target cells for gene delivery. The binding moiety (eg. a ScFv) is
CC pref. external to the receptor for its host cell and fused to the virus
CC direct or indirect by a spacer group. The binding site on the target cell
CC is a cell specific antigen. Fusion C (AAQ64764 fused to AAQ64761) is at
CC the end of the third repetitive unit of the shaft (co-ordinates 31323-4
CC (sequence co-ordinates taken from ADRCOMPGE_1) of the Ad5 fibre. The
CC sequence between the PstI and XhoI sites is unique to the ScFv used. The
CC first 6 amino acid residues of the fusion A protein are from Ad5, the
CC next 4 from the ScFv fragment used. X11 represents the remainder of the
CC ScFv used. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-
CC AUG-2003 to correct OS field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKT 6
|||
Db 3 KKT 5

RESULT 63
AAR55163
ID AAR55163 standard; protein; 11 AA.
XX
AC AAR55163;
XX
DT 25-MAR-2003 (revised)
DT 11-JAN-1995 (first entry)
XX
DE Fragment of retinoic acid receptor RAR-beta.
XX
KW Liver; hap; retinoic acid receptor; steroid; thyroid; hormone; hepatoma;

KW retinoid; antibody.
XX
OS Homo sapiens.
XX
PN US5317090-A.
XX
PD 31-MAY-1994.
XX
PF 11-DEC-1992; 92US-00989902.
XX
PR 16-DEC-1987; 87US-00133687.
PR 17-DEC-1987; 87US-00134130.
PR 20-JUN-1988; 88US-00209009.
PR 30-NOV-1988; 88US-00278136.
PR 30-MAR-1989; 89US-00330405.
PR 21-AUG-1991; 91US-00751612.
PR 30-MAR-1992; 92US-00860577.
XX
PA (INSP) INST PASTEUR.
XX
PI Marchio A, Chambon P, Petkovich M, Krust A, Dejean A, Tiollais P;
PI Brand N, De The HB;
XX
DR WPI; 1994-176333/21.
XX
PT Antibody specific for retinoic acid receptor-beta - useful for detecting,
PT quantifying and identifying agonists and antagonists of retinoid
PT activity.
XX
PS Claim 4; Col 40; 35pp; English.
XX
CC The retinoic acid receptor RAR-beta is encoded by a gene designated hap.
CC The hap gene is transcribed at low level in most human tissues, but the
CC gene is overexpressed in prostate and kidney. Six out of seven hepatoma or
CC hepatoma-derived cell lines express a small hap transcript which is
CC undetectable in normal adult and foetal livers but present in all non-
CC hepatic tissues tested. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NKK 5
 |||
Db 4 NKK 6

RESULT 64
AAR67084
ID AAR67084 standard; peptide; 11 AA.
XX
AC AAR67084;
XX
DT 25-MAR-2003 (revised)
DT 29-JUN-1995 (first entry)

XX
DE Sweet peptide (SW-MB1) contg. proline brackets.
XX
KW Sweet peptide; non-nutrient sweetner; food; drink; dessert; candy;
interaction site; constrained conformation; reduce calorie intake;
sweet tasting papillae; diabetes; mimic; thaumatin; monellin; mabinlin.
XX
OS Synthetic.
XX
PN WO9425482-A1.
XX
PD 10-NOV-1994.
XX
PF 21-APR-1994; 94WO-US004294.
XX
PR 23-APR-1993; 93US-00051741.
PR 29-OCT-1993; 93US-00143364.
XX
PA (EVAN/) EVANS H J.
PA (KINI/) KINI R M.
XX
PI Evans HJ, Kini RM;
XX
DR WPI; 1994-358186/44.
XX
PT Peptide homologue or analogue with constrained conformation - has proline
PT residues flanking the interaction site to impart greater, or more stable,
PT biological activity.
XX
PS Example 2; Page 32; 57pp; English.
XX
CC AAR67077-88 are sweet peptides derived from naturally occurring
CC polypeptides that contain proline or proline/cysteine brackets. These
CC peptides are shortened to form fragments that contain one or more
CC interaction sites of interest. AAR67084-88 are deriv. from mabinlin. The
CC sweet peptides bind to receptors of sweet tasting papillae and induce a
CC sweet sensation. Typically, these peptides are 5000 to 10000 times
CC sweeter than sugar. In comparison, aspartame is only 160 times sweeter
CC than sugar. The peptides are useful as non-nutrient sweetners for food,
CC etc. and are helpful in normal and low calorie diets. They are esp.
CC suitable for people with diabetes. The data collected demonstrates that
CC interaction sites possess activity when present in a polypeptide that
CC differs from the native form. Inclusion of conformation-constraining
CC moieties can have desirable effects on an interaction site. (Also see
CC AAR67011-76 and AAR67089-152 for analogues of other biologically active
CC peptides contg. an interaction site flanked by conformation constraining
CC gps., eg. RGD peptides.) (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 3 RRP 5

RESULT 65
AAR45679
ID AAR45679 standard; protein; 11 AA.
XX
AC AAR45679;
XX
DT 25-MAR-2003 (revised)
DT 25-JUL-1994 (first entry)
XX
DE Fibronectin heparin binding fragment.
XX
KW Cationic antibacterial protein; lipopolysaccharide binding;
KW anticoagulant; granulocytes; RNIP; LPS; sepsis; autoimmune disorder;
KW septic shock; rabbit; CAP18.
XX
OS Synthetic.
XX
PN WO9402589-A1.
XX
PD 03-FEB-1994.
XX
PF 15-JUL-1993; 93WO-US006731.
XX
PR 17-JUL-1992; 92US-00916761.
PR 17-JUL-1992; 92US-00916765.
XX
PA (PANO-) PANORAMA RES INC.
XX
PI Lerrick JW, Wright SC, Hirata M;
XX
DR WPI; 1994-048847/06.
XX
PT Sequences encoding mammalian cationic antibacterial proteins - are
PT homologous to human and rabbit CAP18 sequences and have
PT lipo:polysaccharide binding and anti-coagulation activity.
XX
PS Disclosure; Page 50; 112pp; English.
XX
CC The sequence of CAP18 C-terminal RNIP was compared to that of a number of
CC heparin binding proteins to determine residues important for binding to
CC lipopolysaccharides and inhibiting LPS-mediated activation of macrophage,
CC as well as interfering with the clotting cascade to inhibit coagulation
CC in conditions of disseminated intravascular coagulation. See also
CC AAR45667-81. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
 |||
Db 7 RPR 9

RESULT 66
AAR62627
ID AAR62627 standard; peptide; 11 AA.
XX
AC AAR62627;
XX
DT 25-MAR-2003 (revised)
DT 11-MAY-1995 (first entry)
XX
DE Epidermal growth factor-inhibitor fragment.
XX
KW Epidermal growth factor-inhibitor; therapeutic.
XX
OS Oryctolagus cuniculus.
XX
PN WO9422901-A1.
XX
PD 13-OCT-1994.
XX
PF 04-APR-1994; 94WO-US003675.
XX
PR 02-APR-1993; 93US-00041774.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Strayer DS;
XX
DR WPI; 1994-333107/41.
XX
PT Epidermal growth factor inhibitor protein - capable inhibiting EGF-
PT induced cellular proliferation.
XX
PS Claim 5; Page 33; 43pp; English.
XX
CC The fragment is linked to AAR62628 by at least one peptide bond, and
CC shows sequence homology with AAR62630, the human ras-like protein
CC isolated from teratocarcinoma cells. The resulting epidermal growth
CC factor inhibitor is used in the treatment of disorders in animals
CC (humans) caused by EGF-related rapid cell proliferation e.g. psoriasis,
CC carcinoma, etc., and for the treatment of disorders of the mucous
CC membranes of the body e.g. leukoplakia. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKT 6
|||
Db 8 KKT 10

RESULT 67
AAR46491

ID AAR46491 standard; protein; 11 AA.
XX
AC AAR46491;
XX
DT 25-MAR-2003 (revised)
DT 09-JUL-1994 (first entry)
XX
DE Growth cone membrane p34-A.
XX
KW GAP-43; internal regulatory protein; IRP; neuron; neuronal growth;
KW growth cone membrane; p34; p38.
XX
OS Rattus sp.
XX
PN AU9062068-A.
XX
PD 03-JAN-1991.
XX
PF 31-AUG-1990; 90AU-00062068.
XX
PR 22-DEC-1989; 89US-00465635.
PR 02-JUL-1990; 90US-00546453.
XX
PA (FISH//) FISHMAN M C.
PA (FEDE) FEDEROFF H J.
PA (ZUBE//) ZUBER M X.
PA (STRI//) STRITTMATTER S M.
PA (VALE//) VALENZUELA D.
XX
PI Fishman MC, Federoff HJ, Zuber MX, Strittmatter SM, Valenzuela D;
XX
DR WPI; 1994-049230/07.
XX
PT Recombinant mammalian GAP-43 protein - used to monitor and regulate
PT neuronal growth in animals, pref. humans.
XX
PS Disclosure; Fig 16; 156pp; English.
XX
CC Proteins p34 and p38 were detected in rat growth cone membrane
CC preparations and identified as the alpha and beta subunits, respectively,
CC of the GTP-binding protein, Go. Partial protein sequences were
CC determined: p38-A (AAR46488), p38-B (AAR46489), p38-C (AAR46490), p34-A
CC (AAR46491) and p34-B (AAR46492 or AAR46493). (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TNK 4
|||
Db 9 TNK 11

AAR71762

ID AAR71762 standard; peptide; 11 AA.

XX

AC AAR71762;

XX

DT 25-MAR-2003 (revised)

DT 15-MAY-1995 (first entry)

XX

DE Neurotensin receptor fluorescent probe.

XX

KW Neurotensin; NT; receptor; probe; fluorescent.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Tyr or D-Tyr; and this residue is N-acylated with
FT fluorescent label. See CC below. Also this amino acid can
FT be substituted by Lys or Orn."

XX

PN EP606804-A2.

XX

PD 20-JUL-1994.

XX

PF 27-DEC-1993; 93EP-00403185.

XX

PR 30-DEC-1992; 92CA-02086453.

XX

PA (UYMC-) UNIV MCGILL.

XX

PI Beaudet A, Faure M, Gaudreau P;

XX

DR WPI; 1994-226757/28.

XX

PT New fluorescent markers for neurotensin receptors - useful for in vitro
PT labelling of neurotensin receptors on cell surface and to isolate

PT neurotensin-receptor expressing cells.

XX

PS Claim 2; Page 5; 19pp; English.

XX

CC The invention concerns highly sensitive fluorescent probes which allow
CC for rapid and precise characterisation of neurotensin receptor binding
CC properties on whole cells. The probes are of formula R1-C(=X)-R in which
CC R1 is a fluorophore chosen from fluorescein, rhodamine, Blue
CC fluorescent and Texas red; X is oxygen or sulphur; and R is a neurotensin
CC -type polypeptide sequence containing the core sequence Arg-Arg-Pro-Tyr-
CC Ile-Leu or Arg-Arg-Pro-Trp-Ile-Leu. Specific sequences are given in
CC AAR71745 - AAR71772. The R1-CX- acyl group is linked to the peptide via
CC the N-terminus in position 1. The N-terminal amino acid may also be
CC subst. by Lys or Orn. The present sequence represents one of the claimed
CC peptide sequences for R. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.4e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RRP 10
|||
Db 6 RRP 8

RESULT 69
AAR71761
ID AAR71761 standard; peptide; 11 AA.
XX
AC AAR71761;
XX
DT 25-MAR-2003 (revised)
DT 15-MAY-1995 (first entry)
XX
DE Neurotensin receptor fluorescent probe.
XX
KW Neurotensin; NT; receptor; probe; fluorescent.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "Tyr or D-Tyr; and this residue is N-acylated with
FT fluorescent label. See CC below. Also this amino acid can
FT be substituted by Lys or Orn."
XX
PN EP606804-A2.
XX
PD 20-JUL-1994.
XX
PF 27-DEC-1993; 93EP-00403185.
XX
PR 30-DEC-1992; 92CA-02086453.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Beaudet A, Faure M, Gaudreau P;
XX
DR WPI; 1994-226757/28.
XX
PT New fluorescent markers for neurotensin receptors - useful for in vitro
PT labelling of neurotensin receptors on cell surface and to isolate
PT neurotensin-receptor expressing cells.
XX
PS Claim 2; Page 5; 19pp; English.
XX
CC The invention concerns highly sensitive fluorescent probes which allow
CC for rapid and precise characterisation of neurotensin receptor binding
CC properties on whole cells. The probes are of formula R1-C(=X)-R in which
CC R1 is a fluorophore chosen from fluorescein, rhodamine, Blue
CC fluorescent and Texas red; X is oxygen or sulphur; and R is a neurotensin
CC -type polypeptide sequence containing the core sequence Arg-Arg-Pro-Tyr-
CC Ile-Leu or Arg-Arg-Pro-Trp-Ile-Leu. Specific sequences are given in
CC AAR71745 - AAR71772. The R1-CX- acyl group is linked to the peptide via
CC the N-terminus in position 1. The N-terminal amino acid may also be
CC substd. by Lys or Orn. The present sequence represents one of the claimed

CC peptide sequences for R. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 6 RRP 8

RESULT 70

AAR71764

ID AAR71764 standard; peptide; 11 AA.

XX

AC AAR71764;

XX

DT 25-MAR-2003 (revised)

DT 15-MAY-1995 (first entry)

XX

DE Neurotensin receptor fluorescent probe.

XX

KW Neurotensin; NT; receptor; probe; fluorescent.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Tyr or D-Tyr; and this residue is N-acylated with
FT fluorescent label. See CC below. Also this amino acid can
FT be substituted by Lys or Orn."

FT Modified-site 4

FT /label= Orn

XX

PN EP606804-A2.

XX

PD 20-JUL-1994.

XX

PF 27-DEC-1993; 93EP-00403185.

XX

PR 30-DEC-1992; 92CA-02086453.

XX

PA (UYMC-) UNIV MCGILL.

XX

PI Beaudet A, Faure M, Gaudreau P;

XX

DR WPI; 1994-226757/28.

XX

PT New fluorescent markers for neurotensin receptors - useful for in vitro
PT labelling of neurotensin receptors on cell surface and to isolate
PT neurotensin-receptor expressing cells.

XX

PS Claim 2; Page 5; 19pp; English.

XX

CC The invention concerns highly sensitive fluorescent probes which allow

CC for rapid and precise characterisation of neuropeptide receptor binding
CC properties on whole cells. The probes are of formula R1-C(=X)-R in which
CC R1 is a fluorophore chosen from fluorescein, rhodamine, Blue
CC fluorescent and Texas red; X is oxygen or sulphur; and R is a neuropeptide
CC -type polypeptide sequence containing the core sequence Arg-Arg-Pro-Tyr-
CC Ile-Leu or Arg-Arg-Pro-Trp-Ile-Leu. Specific sequences are given in
CC AAR71745 - AAR71772. The R1-CX- acyl group is linked to the peptide via
CC the N-terminus in position 1. The N-terminal amino acid may also be
CC subst. by Lys or Orn. The present sequence represents one of the claimed
CC peptide sequences for R. (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 6 RRP 8

RESULT 71

AAR71763

ID AAR71763 standard; peptide; 11 AA.

XX

AC AAR71763;

XX

DT 25-MAR-2003 (revised)

DT 15-MAY-1995 (first entry)

XX

DE Neurotensin receptor fluorescent probe.

XX

KW Neurotensin; NT; receptor; probe; fluorescent.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Tyr or D-Tyr; and this residue is N-acylated with
FT fluorescent label. See CC below. Also this amino acid can
FT be substituted by Lys or Orn."

FT Modified-site 4

FT /label= Orn

XX

PN EP606804-A2.

XX

PD 20-JUL-1994.

XX

PF 27-DEC-1993; 93EP-00403185.

XX

PR 30-DEC-1992; 92CA-02086453.

XX

PA (UYMC-) UNIV MCGILL.

XX

PI Beaudet A, Faure M, Gaudreau P;

XX

DR WPI; 1994-226757/28.

XX

PT New fluorescent markers for neuropeptides receptors - useful for in vitro
PT labelling of neuropeptides receptors on cell surface and to isolate
PT neuropeptides-receptor expressing cells.

XX

PS Claim 2; Page 5; 19pp; English.

XX

CC The invention concerns highly sensitive fluorescent probes which allow
CC for rapid and precise characterisation of neuropeptides receptor binding
CC properties on whole cells. The probes are of formula R1-C(=X)-R in which
CC R1 is a fluorophore chosen from fluorescein, rhodamine, Blue
CC fluorescent and Texas red; X is oxygen or sulphur; and R is a neuropeptides
CC -type polypeptide sequence containing the core sequence Arg-Arg-Pro-Tyr-
CC Ile-Leu or Arg-Arg-Pro-Trp-Ile-Leu. Specific sequences are given in
CC AAR71745 - AAR71772. The R1-CX- acyl group is linked to the peptide via
CC the N-terminus in position 1. The N-terminal amino acid may also be
CC substd. by Lys or Orn. The present sequence represents one of the claimed
CC peptide sequences for R. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||

Db 6 RRP 8

RESULT 72

AAR54763

ID AAR54763 standard; peptide; 11 AA.

XX

AC AAR54763; .

XX

DT 25-MAR-2003 (revised)

DT 02-DEC-1994 (first entry)

XX

DE Plasminogen analog with basic amino acid in cleavage site.

XX

KW Plasminogen; blood-clotting; cleavage site; thrombin; protease; enzyme;

KW thrombosis; infarction; coagulation; cancer.

XX

OS Homo sapiens.

XX

PN WO9410318-A1.

XX

PD 11-MAY-1994.

XX

PF 28-OCT-1993; 93WO-GB002219.

XX

PR 29-OCT-1992; 92GB-00022758.

XX

PA (BRB1-) BRITISH BIO-TECHNOLOGY LTD.

XX

PI Gilbert RJ, Hunter MG, Dawson KM;
XX
DR WPI; 1994-167473/20.
XX
PT New thrombin activatable plasminogen analogues - having a basic amino
PT acid residue in the cleavage site to provide more rapid cleavage and
PT improved activity.
XX
PS Claim 13; Page 26; 38pp; English.
XX
CC This peptide sequence corresponds to a cleavage site present in a
CC plasminogen analog which enables the protein to be cleaved more rapidly
CC by thrombin. The plasminogen analogs are used for prophylaxis and/or
CC treatment of conditions caused by an imbalance between clotting and
CC fibrinolysis. They can be used to treat e.g. infarction, thrombosis and
CC coagulation imbalances associated with cancer. The analogs can be
CC prepared by chemical synthesis or preferably by recombinant DNA
CC techniques. The analogs are prepared by mutagenesis of cDNA and
CC expression in CHO cell cultures. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 7 RPR 9

RESULT 73
AAR46502
ID AAR46502 standard; protein; 11 AA.
XX
AC AAR46502;
XX
DT 09-JUL-1994 (first entry)
XX
DE Growth cone membrane p34-A.
XX
KW GAP-43; internal regulatory protein; IRP; neuron; neuronal growth;
KW growth cone membrane; p34; p38.
XX
OS Rattus sp.
XX
PN AU9347435-A.
XX
PD 23-DEC-1993.
XX
PF 17-SEP-1993; 93AU-00047435.
XX
PR 22-DEC-1989; 89US-00465635.
PR 02-JUL-1990; 90US-00546453.
XX
PA (FISH/) FISHMAN M C.

PA (FEDE/) FEDEROFF H J.
PA (ZUBE/) ZUBER M X.
PA (STRI/) STRITTMATTER S M.
PA (VALE/) VALENZUELA D.
XX
PI Fishman MC, Federoff HJ, Zuber MX, Strittmatter SM, Valenzuela D;
XX
DR WPI; 1994-049278/07.
XX
PT Recombinant mammalian GAP-43 protein - used to monitor and regulate
PT neuronal growth in animals, pref. humans.
XX
PS Disclosure; Fig 16; 156pp; English.
XX
CC Proteins p34 and p38 were detected in rat growth cone membrane
CC preparations and identified as the alpha and beta subunits, respectively,
CC of the GTP-binding protein, Go. Partial protein sequences were
CC determined: p38-A (AAR46499), p38-B (AAR46500), p38-C (AAR46501), p34-A
CC (AAR46502) and p34-B (AAR46503 or AAR46504)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TNK 4
|||
Db 9 TNK 11

RESULT 74
AAR70293
ID AAR70293 standard; peptide; 11 AA.
XX
AC AAR70293;
XX
DT 14-NOV-1995 (first entry)
XX
DE Subpeptide 7N1 of thrombospondin 1 (TS1) binding peptide C7.
XX
KW Thrombospondin 1; TS1; receptor; cell-adhesion.
XX
OS Synthetic.
XX
PN US5399667-A.
XX
PD 21-MAR-1995.
XX
PF 05-MAR-1993; 93US-00029333.
XX
PR 05-MAR-1993; 93US-00029333.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Kosfeld MD, Frazier WA;
XX

DR WPI; 1995-130736/17.
XX
PT Thrombospondin receptor binding peptide(s) - comprise tri:peptide
PT sequence Val-Val-Met (VVM).
XX
PS Disclosure; Fig 1A; 25pp; English.
XX
CC AAR70292-300 are synthetic subpeptides which were derived from peptide C7
CC of the cell binding domain (CBD) of the thrombospondin 1 (TS1) receptor.
CC These peptides were synthesised and used in a cell adhesion assay.
CC Subpeptides 7N1, 7N2, 7N2-1, 7N2-2, 7N3 and 7N3-2 were used to further
CC locate the active sequence(s). The binding activity of this subpeptide in
CC relation to peptides C7, 7C, 7N and the 7N subpeptide derivatives 7N2,
CC 7N2-1, 7N2-2, 7N3, and 7N3-2 is as follows: 7N>7N3>7N2>7N2-2>7N3-
CC 2>7C, 7N1, 7N2-1 (AAR70291>292>297>294>296>299>300,293,295)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 KTG 7
|||
Db 9 KTG 11

RESULT 75
AAR70594
ID AAR70594 standard; peptide; 11 AA.
XX
AC AAR70594;
XX
DT 14-FEB-1996 (first entry)
XX
DE HIV(B35)-19, human immunodeficiency virus epitope.
XX
KW HLA; human lymphocyte antigen; HIV; human immunodeficiency virus;
KW binding peptide; induce killer cell; prevention; treatment; AIDS;
KW autoimmune disease syndrome; vaccine.
XX
OS Human immunodeficiency virus.
XX
PN WO9511255-A1.
XX
PD 27-APR-1995.
XX
PF 19-OCT-1994; 94WO-JP001756.
XX
PR 19-OCT-1993; 93JP-00261302.
XX
PA (AJIN) AJINOMOTO KK.
XX
PI Takiguchi M, Miwa K;
XX
DR WPI; 1995-170188/22.
XX

PT HLA-binding peptide fragments from HIV proteins - induce killer cells
PT which target HIV-infected cells and can be incorporated into anti-HIV
PT vaccines.

XX

PS Example 1; Page 10; 61pp; Japanese.

XX

CC AAR70594 is a peptide fragment derived from an HIV (Human
CC Immunodeficiency Virus) pol protein (residues 587-596) and is capable of
CC binding to a human lymphocyte antigen. The peptide can induce killer
CC cells which target HIV-infected cells. It is also useful in the
CC prevention and treatment of HIV and AIDS. Anti-HIV vaccines may
CC incorporate the peptides, or may incorporate a vector (such as vaccinia
CC or BCG) contg. DNA encoding the peptides

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KTG 7

|||

Db 7 KTG 9

Search completed: April 8, 2004, 15:39:55

Job time : 46.3077 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:08 ; Search time 11.3077 Seconds
(without alignments)
50.221 Million cell updates/sec

Title: US-09-787-443A-9
Perfect score: 11
Sequence: 1 ATNKKTGRRPR 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8542

Minimum DB seq length: 11
Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
	No.	Score	Match	Length	DB ID	
1	5	45.5	11	4	US-09-630-250B-15	Sequence 15, Appl
2	4	36.4	11	3	US-09-208-966-55	Sequence 55, Appl
3	4	36.4	11	3	US-09-208-966-57	Sequence 57, Appl
4	4	36.4	11	3	US-09-044-411-7	Sequence 7, Appl
5	4	36.4	11	3	US-09-133-062D-29	Sequence 29, Appl
6	4	36.4	11	4	US-09-802-109A-7	Sequence 7, Appl
7	4	36.4	11	4	US-09-630-250B-16	Sequence 16, Appl
8	4	36.4	11	4	US-09-775-052A-55	Sequence 55, Appl
9	4	36.4	11	4	US-09-775-052A-57	Sequence 57, Appl
10	4	36.4	11	6	5223254-12	Patent No. 5223254
11	3	27.3	11	1	US-07-666-719-18	Sequence 18, Appl

12	3	27.3	11	1	US-07-718-274A-23	Sequence 23, Appl
13	3	27.3	11	1	US-07-755-161A-9	Sequence 9, Appl
14	3	27.3	11	1	US-07-891-174-9	Sequence 9, Appl
15	3	27.3	11	1	US-07-912-900-2	Sequence 2, Appl
16	3	27.3	11	1	US-07-912-900-13	Sequence 13, Appl
17	3	27.3	11	1	US-07-912-900-15	Sequence 15, Appl
18	3	27.3	11	1	US-08-029-333-21	Sequence 21, Appl
19	3	27.3	11	1	US-08-149-106-23	Sequence 23, Appl
20	3	27.3	11	1	US-07-841-997A-34	Sequence 34, Appl
21	3	27.3	11	1	US-08-037-486-6	Sequence 6, Appl
22	3	27.3	11	1	US-08-336-087-4	Sequence 4, Appl
23	3	27.3	11	1	US-08-298-021-23	Sequence 23, Appl
24	3	27.3	11	1	US-07-609-716-15	Sequence 15, Appl
25	3	27.3	11	1	US-08-178-570-75	Sequence 75, Appl
26	3	27.3	11	1	US-08-041-774-2	Sequence 2, Appl
27	3	27.3	11	1	US-08-217-188A-35	Sequence 35, Appl
28	3	27.3	11	1	US-08-217-188A-60	Sequence 60, Appl
29	3	27.3	11	1	US-08-170-095B-6	Sequence 6, Appl
30	3	27.3	11	1	US-08-285-309-2	Sequence 2, Appl
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34	3	27.3	11	1	US-08-378-761A-68	Sequence 68, Appl
35	3	27.3	11	1	US-08-378-761A-70	Sequence 70, Appl
36	3	27.3	11	1	US-08-313-075A-12	Sequence 12, Appl
37	3	27.3	11	1	US-08-313-075A-14	Sequence 14, Appl
38	3	27.3	11	1	US-08-485-286-68	Sequence 68, Appl
39	3	27.3	11	1	US-08-485-286-70	Sequence 70, Appl
40	3	27.3	11	1	US-08-344-636-15	Sequence 15, Appl
41	3	27.3	11	1	US-08-344-636-18	Sequence 18, Appl
42	3	27.3	11	1	US-08-256-771-32	Sequence 32, Appl
43	3	27.3	11	1	US-08-396-866-6	Sequence 6, Appl
44	3	27.3	11	1	US-08-336-343A-24	Sequence 24, Appl
45	3	27.3	11	1	US-08-469-582-7	Sequence 7, Appl
46	3	27.3	11	1	US-08-469-582-19	Sequence 19, Appl
47	3	27.3	11	1	US-08-479-400-4	Sequence 4, Appl
48	3	27.3	11	1	US-08-687-226-35	Sequence 35, Appl
49	3	27.3	11	1	US-08-687-226-60	Sequence 60, Appl
50	3	27.3	11	1	US-08-687-226-67	Sequence 67, Appl
51	3	27.3	11	1	US-08-615-181-88	Sequence 88, Appl
52	3	27.3	11	1	US-08-477-509B-36	Sequence 36, Appl
53	3	27.3	11	1	US-08-082-269D-5	Sequence 5, Appl
54	3	27.3	11	1	US-08-082-269D-8	Sequence 8, Appl
55	3	27.3	11	1	US-08-259-550A-5	Sequence 5, Appl
56	3	27.3	11	1	US-08-290-301-34	Sequence 34, Appl
57	3	27.3	11	1	US-08-381-984-32	Sequence 32, Appl
58	3	27.3	11	2	US-08-669-721-17	Sequence 17, Appl
59	3	27.3	11	2	US-08-669-721-18	Sequence 18, Appl
60	3	27.3	11	2	US-08-669-721-19	Sequence 19, Appl
61	3	27.3	11	2	US-08-669-721-20	Sequence 20, Appl
62	3	27.3	11	2	US-08-508-664-13	Sequence 13, Appl
63	3	27.3	11	2	US-08-701-124-19	Sequence 19, Appl
64	3	27.3	11	2	US-08-473-025-12	Sequence 12, Appl
65	3	27.3	11	2	US-08-502-046-2	Sequence 2, Appl
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74	3	27.3	11	2	US-09-207-621-77	Sequence 77, Appl
75	3	27.3	11	2	US-08-645-193B-55	Sequence 55, Appl
76	3	27.3	11	2	US-08-532-818-77	Sequence 77, Appl
77	3	27.3	11	2	US-08-997-080-7	Sequence 7, Appli
78	3	27.3	11	2	US-08-997-362-7	Sequence 7, Appli
79	3	27.3	11	2	US-09-090-567-4	Sequence 4, Appli
80	3	27.3	11	3	US-08-873-970-7	Sequence 7, Appli
81	3	27.3	11	3	US-08-369-643-75	Sequence 75, Appl
82	3	27.3	11	3	US-09-076-646-4	Sequence 4, Appli
83	3	27.3	11	3	US-08-482-085B-36	Sequence 36, Appl
84	3	27.3	11	3	US-08-904-446A-9	Sequence 9, Appli
85	3	27.3	11	3	US-08-802-981-147	Sequence 147, App
86	3	27.3	11	3	US-09-130-225-19	Sequence 19, Appl
87	3	27.3	11	3	US-08-667-725B-35	Sequence 35, Appl
88	3	27.3	11	3	US-08-667-725B-60	Sequence 60, Appl
89	3	27.3	11	3	US-09-231-797-77	Sequence 77, Appl
90	3	27.3	11	3	US-08-934-224-77	Sequence 77, Appl
91	3	27.3	11	3	US-09-322-911-25	Sequence 25, Appl
92	3	27.3	11	3	US-08-933-843-77	Sequence 77, Appl
93	3	27.3	11	3	US-08-475-411A-15	Sequence 15, Appl
94	3	27.3	11	3	US-09-007-748-35	Sequence 35, Appl
95	3	27.3	11	3	US-09-007-748-60	Sequence 60, Appl
96	3	27.3	11	3	US-08-934-223-77	Sequence 77, Appl
97	3	27.3	11	3	US-09-095-855-7	Sequence 7, Appli
98	3	27.3	11	3	US-09-273-565-54	Sequence 54, Appl
99	3	27.3	11	3	US-08-836-075A-109	Sequence 109, App
100	3	27.3	11	3	US-08-836-075A-110	Sequence 110, App

ALIGNMENTS

RESULT 1

US-09-630-250B-15
; Sequence 15, Application US/09630250B
; Patent No. 6624129
; GENERAL INFORMATION:
; APPLICANT: Borch, Kim
; APPLICANT: Vind, Jesper
; APPLICANT: Svendsen, Allan
; APPLICANT: Hlakier, Dorte
; APPLICANT: Patkar, Shamkant
; APPLICANT: Bojsen, Kirsten
; TITLE OF INVENTION: Lipase Variant
; FILE REFERENCE: 5469.204-US
; CURRENT APPLICATION NUMBER: US/09/630,250B
; CURRENT FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 11
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-630-250B-15

Query Match 45.5%; Score 5; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRRPR 11
|||||
Db 5 GRRPR 9

RESULT 2

US-09-208-966-55

; Sequence 55, Application US/09208966
; Patent No. 6221355
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48881/1742
; CURRENT APPLICATION NUMBER: US/09/208,966
; CURRENT FILING DATE: 1998-12-10
; EARLIER APPLICATION NUMBER: 60/082,402
; EARLIER FILING DATE: 1998-04-20
; EARLIER APPLICATION NUMBER: 60/069,012
; EARLIER FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human
US-09-208-966-55

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
|||||
Db 6 RRPR 9

RESULT 3

US-09-208-966-57

; Sequence 57, Application US/09208966
; Patent No. 6221355
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48881/1742
; CURRENT APPLICATION NUMBER: US/09/208,966
; CURRENT FILING DATE: 1998-12-10
; EARLIER APPLICATION NUMBER: 60/082,402
; EARLIER FILING DATE: 1998-04-20

; EARLIER APPLICATION NUMBER: 60/069,012
; EARLIER FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human
US-09-208-966-57

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
Db 6 RRPR 9

RESULT 4
US-09-044-411-7
; Sequence 7, Application US/09044411A
; Patent No. 6258774
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/044,411A
; CURRENT FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: Same as Sequence ID 2, but with a substitution of
; Patent No. 6258774
; OTHER INFORMATION: Gln to Pro.
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (10)
; OTHER INFORMATION: Cys(biotin)
; FEATURE:
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.
; FEATURE:
; OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-044-411-7

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
Db 4 RRPR 7

RESULT 5
US-09-133-062D-29
; Sequence 29, Application US/09133062D
; Patent No. 6258776
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A
; APPLICANT: Millward, Thomas A
; TITLE OF INVENTION: Calcium Regulated Kinase
; FILE REFERENCE: 30110
; CURRENT APPLICATION NUMBER: US/09/133,062D
; CURRENT FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: GB 9717089.8
; PRIOR FILING DATE: 1997-08-12
; PRIOR APPLICATION NUMBER: GB 9717499.9
; PRIOR FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic peptide
; OTHER INFORMATION: internal peptide
US-09-133-062D-29

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKTG 7
Db 4 KKTG 7

RESULT 6
US-09-802-109A-7
; Sequence 7, Application US/09802109A
; Patent No. 6617306
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/802,109A
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US/09/044,411
; PRIOR FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: Same as Sequence ID 2, but with a substitution of
; Patent No. 6617306

; OTHER INFORMATION: Gln to Pro.
;
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (10)
; OTHER INFORMATION: Cys(biotin)
;
; FEATURE:
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.
;
; OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-802-109A-7

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
|||
Db 4 RRPR 7

RESULT 7

US-09-630-250B-16
; Sequence 16, Application US/09630250B
; Patent No. 6624129
; GENERAL INFORMATION:
; APPLICANT: Borch, Kim
; APPLICANT: Vind, Jesper
; APPLICANT: Svendsen, Allan
; APPLICANT: Hlakier, Dorte
; APPLICANT: Patkar, Shamkant
; APPLICANT: Bojsen, Kirsten
; TITLE OF INVENTION: Lipase Variant
; FILE REFERENCE: 5469.204-US
; CURRENT APPLICATION NUMBER: US/09/630,250B
; CURRENT FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
;
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-630-250B-16

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRRP 10
|||
Db 8 GRRP 11

RESULT 8

US-09-775-052A-55
; Sequence 55, Application US/09775052A

; Patent No. 6645501
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48881/1742
; CURRENT APPLICATION NUMBER: US/09/775,052A
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/208,966
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,012
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human
US-09-775-052A-55

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
Db 6 RRPR 9

RESULT 9
US-09-775-052A-57
; Sequence 57, Application US/09775052A
; Patent No. 6645501
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48881/1742
; CURRENT APPLICATION NUMBER: US/09/775,052A
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/208,966
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,012
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human
US-09-775-052A-57

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
Db 6 RRPR 9

RESULT 10

5223254-12

; Patent No. 5223254

; APPLICANT: PARADISO, PETER R.; HILDRETH, STEPHEN W.; HU,

; BRANDA T.; MARTIN-GALLARDO, ANTONIA; ARUMUGHAM, RASAPPA

; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES

; NUMBER OF SEQUENCES: 17

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/247,017

; FILING DATE: 20-SEP-1988

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 102,180

; FILING DATE: 29-SEP-1987

; SEQ ID NO:12:

; LENGTH: 11

5223254-12

Query Match 36.4%; Score 4; DB 6; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGRR 9

||||

Db 4 TGRR 7

RESULT 11

US-07-666-719-18

; Sequence 18, Application US/07666719

; Patent No. 5247067

; GENERAL INFORMATION:

; APPLICANT: ARIMA, Terukatsu

; APPLICANT: YAMADA, Kyoko

; APPLICANT: HATANAKA, Tadashi

; APPLICANT: NAMBA, Toshihiko

; APPLICANT: TSUJI, Masao

; TITLE OF INVENTION: PEPTIDE AND ITS USE

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT

; STREET: 1755 Jefferson Davis Highway, Fourth Floor

; CITY: Arlington

; STATE: Virginia

; COUNTRY: US

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/666,719

; FILING DATE: 19910422

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Oblon, No. 5247067man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 363-264-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-5940
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-07-666-719-18

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NKK 5
 |||
Db 7 NKK 9

RESULT 12

US-07-718-274A-23

; Sequence 23, Application US/07718274A
; Patent No. 5284756
; GENERAL INFORMATION:
; APPLICANT: Grinna, Lynn
; APPLICANT: Parsons, Thomas F.
; APPLICANT: Theofan, Georgia
; TITLE OF INVENTION: Osteogenic Factor
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/718,274A
; FILING DATE: 19910620
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/415,555
; FILING DATE: 04-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/256,034

;
; FILING DATE: 11-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/9430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-718-274A-23

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATN 3
 |||
Db 2 ATN 4

RESULT 13

US-07-755-161A-9

;
; Sequence 9, Application US/07755161A
; Patent No. 5304633
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/755,161A
; FILING DATE: 19910905
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367

; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 10
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 10 connected by disulfide
bond with
; OTHER INFORMATION: thiol group of Cys residue at location 35 of SEQ ID
NO. 8"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-9

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
|||
Db 1 GRR 3

RESULT 14

US-07-891-174-9

; Sequence 9, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:

;
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
;
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
;
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
;
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 10
;
; IDENTIFICATION METHOD:
;
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 10 connected by disulfide
bond with
; OTHER INFORMATION: thiol group of Cys residue at location 35 of SEQ ID
NO. 8"
;
; PUBLICATION INFORMATION:
;
; AUTHORS:
;
; TITLE:
;
; JOURNAL:
;
; VOLUME:
;
; ISSUE:
;
; PAGES:
;
; DATE:
;
; DOCUMENT NUMBER:
;
; FILING DATE:
;
; PUBLICATION DATE:
;
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-9

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
|||
Db 1 GRR 3

RESULT 15

US-07-912-900-2

; Sequence 2, Application US/07912900

; Patent No. 5349125

; GENERAL INFORMATION:

; APPLICANT: Holton, Timothy A.

; APPLICANT: Cornish, Edwina C.

; APPLICANT: Kovacic, Filippa

; APPLICANT: Tanaka, Yoshikazu

; APPLICANT: Lester, Diane R.

; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID

; TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR

NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/912,900
FILING DATE: 19920713
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8633
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-912-900-2

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Query Match           27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 3.1e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy          7 GRR 9
           |||
Db          5 GRR 7

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RESULT 16
US-07-912-900-13
; Sequence 13, Application US/07912900
; Patent No. 5349125
; GENERAL INFORMATION:
; APPLICANT: Holton, Timothy A.
; APPLICANT: Cornish, Edwina C.
; APPLICANT: Kovacic, Filippa
; APPLICANT: Tanaka, Yoshikazu
; APPLICANT: Lester, Diane R.
; TITLE OF INVENTION: GENETIC SEQUE
; TITLE OF INVENTION: PATHWAY ENZYME
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/912,900
FILING DATE: 19920713
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8633
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-07-912-900-13

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
Db 5 GRR 7

RESULT 17

US-07-912-900-15

Sequence 15- Application

Patent No. 5349125

GENERAL INFORMATION

ABPLICANT: Holton, Timothy A

APPLICANT: HOLLOWAY, Timothy R.

APPLICANT: CORNISH

APPLICANT: Rovacic, Filippa

APPLICANT: Tanaka, Toshihiko

APPLICANT: Lester, Diane R.

1. TITLE OF INVENTION: GENETIC SELECTION

; TITLE OF INVENTION: PATHWAY E
NUMBER OF SEQUENCES 26

; NUMBER OF SEQUENCES: 29
; NAME OF SOURCE: ADDRESS

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Scully, Scott, M

; STREET: 400 Garden City Pla

; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/912,900
; FILING DATE: 19920713
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8633
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

US-07-912-900-15

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
|||
Db 5 GRR 7

RESULT 18

US-08-029-333-21

; Sequence 21, Application US/08029333

; Patent No. 5399667

; GENERAL INFORMATION:

; APPLICANT: Frazier, William A.

; APPLICANT: Kosfeld, Minh D.

; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides

; NUMBER OF SEQUENCES: 47

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG

; STREET: 800 N. Lindbergh Blvd.

; CITY: St. Louis

; STATE: Missouri

; COUNTRY: USA

; ZIP: 63167

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/029,333
; FILING DATE: 19930305
; CLASSIFICATION: 530
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24(982)A
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 694-3117
; TELEFAX: (314) 694-5435
;
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-029-333-21

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KTG 7
|||
Db 9 KTG 11

RESULT 19
US-08-149-106-23
;
; Sequence 23, Application US/08149106
; Patent No. 5411941
;
; GENERAL INFORMATION:
; APPLICANT: Grinna, Lynn
; APPLICANT: Parsons, Thomas F.
; APPLICANT: Theofan, Georgia
; TITLE OF INVENTION: Osteogenic Factor
; NUMBER OF SEQUENCES: 63
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,106

;
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/415,555
; FILING DATE: 04-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/256,034
; FILING DATE: 11-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/9430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-149-106-23

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATN 3
|||
Db 2 ATN 4

RESULT 20
US-07-841-997A-34
; Sequence 34, Application US/07841997A
; Patent No. 5422254
; GENERAL INFORMATION:
; APPLICANT: Londesborough, John
; APPLICANT: Vuorio, Outi
; TITLE OF INVENTION: A method to increase the trehalose content
; TITLE OF INVENTION: of organisms by transforming them with the
; TITLE OF INVENTION: structural genes for the short and long chains
; TITLE OF INVENTION: yeast trehalose synthase.
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Alko Ltd.
; STREET: PO Box 350
; CITY: Helsinki
; STATE: -
; COUNTRY: Finland
; ZIP: SF-00101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WP5.1 file exported as DOS text file

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/841,997A
; FILING DATE: 19920228
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/836,021
; FILING DATE: February 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary E. Gormley
; REGISTRATION NUMBER: 34409
; REFERENCE/DOCKET NUMBER: 920085A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)659-2930
; TELEFAX: (202)887-0357
; TELEX: 440142
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; HYPOTHETICAL: No
; FRAGMENT TYPE: N-terminal

US-07-841-997A-34

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TNK 4
|||
Db 9 TNK 11

RESULT 21
US-08-037-486-6
; Sequence 6, Application US/08037486
; Patent No. 5470831
; GENERAL INFORMATION:
; APPLICANT: Whitman, Russell B.
; APPLICANT: Wohl, Robert
; APPLICANT: Duff, Ronald G.
; TITLE OF INVENTION: Angiogenic Peptides
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: N.Y.
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/037,486
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/631,823
FILING DATE: 21-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7142-004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212 869-9741
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide

US-08-037-486-6

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 6 RPR 8

RESULT 22

US-08-336-087-4

; Sequence 4, Application US/08336087
; Patent No. 5503829
; GENERAL INFORMATION:
; APPLICANT: Ladant, Daniel
; APPLICANT: Leclerc, Claude
; APPLICANT: Sebo, Peter
; APPLICANT: Ullmann, Agnes
; TITLE OF INVENTION: Recombinant Mutants for Inducing
; TITLE OF INVENTION: Specific Immune Responses
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

;
; APPLICATION NUMBER: US/08/336,087
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/011,644
; FILING DATE: 29-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495-0109-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-336-087-4

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TNK 4
 |||
Db 7 TNK 9

RESULT 23
US-08-298-021-23
; Sequence 23, Application US/08298021
; Patent No. 5508263
; GENERAL INFORMATION:
; APPLICANT: Grinna, Lynn
; APPLICANT: Parsons, Thomas F.
; APPLICANT: Theofan, Georgia
; TITLE OF INVENTION: Heterodimeric Osteogenic Factor
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-64023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/298,021
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

;
; APPLICATION NUMBER: US 08/149,106
; FILING DATE: 11-OCT-1993
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/718,274
; FILING DATE: 20-JUN-1991
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/415,555
; FILING DATE: 04-OCT-1989
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/256,034
; FILING DATE: 11-OCT-1988
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/32196
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
;
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-298-021-23

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATN 3
 |||
Db 2 ATN 4

RESULT 24

US-07-609-716-15

;
; Sequence 15, Application US/07609716
;
; Patent No. 5514581
;
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A.
; APPLICANT: Cappello, Joseph
;
; TITLE OF INVENTION: Functional Recombinantly Prepared
;
; TITLE OF INVENTION: Synthetic Protein Polymer
;
; NUMBER OF SEQUENCES: 118
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
;
; STREET: Four Embarcadero Center, Suite 3400
;
; CITY: San Francisco
;
; STATE: CA
;
; COUNTRY: US
;
; ZIP: 94111
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/609,716
FILING DATE: 06-NOV-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-55186-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-609-716-15

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGR 8
Db 3 TGR 5

RESULT 25
US-08-178-570-75
; Sequence 75, Application US/08178570
; Patent No. 5532167
; GENERAL INFORMATION:
; APPLICANT: Lewis C. Cantley
; APPLICANT: Zhou Song yang
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/178,570
; FILING DATE: JANUARY 7, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.

; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-178-570-75

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 2 RRP 4

RESULT 26

US-08-041-774-2

; Sequence 2, Application US/08041774
; Patent No. 5550114
; GENERAL INFORMATION:
; APPLICANT: Strayer, David S.
; TITLE OF INVENTION: EPIDERMAL GROWTH FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/041,774
; FILING DATE: 19930402
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Zivin, No. 5550114man H.
; REGISTRATION NUMBER: 25,385
; REFERENCE/DOCKET NUMBER: 2560/42559
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: internal

US-08-041-774-2

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKT 6
|||
Db 8 KKT 10

RESULT 27

US-08-217-188A-35

; Sequence 35, Application US/08217188A
; Patent No. 5554724
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,188A
; FILING DATE: 24-MARCH-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5554724man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-217-188A-35

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KTG 7
|||
Db 4 KTG 6

RESULT 28

US-08-217-188A-60

; Sequence 60, Application US/08217188A
; Patent No. 5554724

; GENERAL INFORMATION:

; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry

; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 62

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/217,188A
; FILING DATE: 24-MARCH-1994
; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, No. 5554724man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 60:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-217-188A-60

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KTG 7
|||
Db 1 KTG 3

RESULT 29

US-08-170-095B-6

; Sequence 6, Application US/08170095B
; Patent No. 5563254
; GENERAL INFORMATION:
; APPLICANT: Hoffman, Stephen J.
; APPLICANT: Nagai, Kiyoshi
; TITLE OF INVENTION: Blood Substitutes
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 2545 Central Avenue
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.0.1
; SOFTWARE: Microsoft Word 5.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,095B
; FILING DATE: December 20, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5563254ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: Hoffman 2A/CONT2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-541-3322
; TELEFAX: 303-444-3013
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown to applicant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: no

US-08-170-095B-6

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9

RESULT 30
US-08-285-309-2
; Sequence 2, Application US/08285309
; Patent No. 5569832
; GENERAL INFORMATION:
; APPLICANT: Holton, Timothy A.
; APPLICANT: Cornish, Edwina C.
; APPLICANT: Kovacic, Filippa
; APPLICANT: Tanaka, Yoshikazu
; APPLICANT: Lester, Diane R.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
; TITLE OF INVENTION: HYDROXYLASE AND USES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/285,309
; FILING DATE: 03-AUG-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8633Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-285-309-2

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 31

US-08-285-309-13

; Sequence 13, Application US/08285309

; Patent No. 5569832

; GENERAL INFORMATION:

; APPLICANT: Holton, Timothy A.

; APPLICANT: Cornish, Edwina C.

; APPLICANT: Kovacic, Filippa

; APPLICANT: Tanaka, Yoshikazu

; APPLICANT: Lester, Diane R.

; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-

; TITLE OF INVENTION: HYDROXYLASE AND USES

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Scully, Scott, Murphy & Presser

; STREET: 400 Garden City Plaza

; CITY: Garden City

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 11530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/285,309

; FILING DATE: 03-AUG-1994

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: DiGiglio, Frank S.

; REGISTRATION NUMBER: 31,346

; REFERENCE/DOCKET NUMBER: 8633Z

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (516) 742-4343

; TELEFAX: (516) 742-4366

; TELEX: 230 901 SANS UR

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-285-309-13

Query Match 27.3%; Score 3; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
|||

Db 5 GRR 7

RESULT 32
US-08-285-309-15
; Sequence 15, Application US/08285309
; Patent No. 5569832
; GENERAL INFORMATION:
; APPLICANT: Holton, Timothy A.
; APPLICANT: Cornish, Edwina C.
; APPLICANT: Kovacic, Filippa
; APPLICANT: Tanaka, Yoshikazu
; APPLICANT: Lester, Diane R.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
; TITLE OF INVENTION: HYDROXYLASE AND USES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/285,309
; FILING DATE: 03-AUG-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8633Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-285-309-15

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
|||
Db 5 GRR 7

RESULT 33
US-08-313-681A-25

; Sequence 25, Application US/08313681A
; Patent No. 5618675
; GENERAL INFORMATION:
; APPLICANT: Lerrick, James W.
; APPLICANT: Wright, Susan C.
; APPLICANT: Hirata, Mishimasa
; TITLE OF INVENTION: Human Cationic Proteins Having
; TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,681A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15325-9-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-313-681A-25

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
 |||
Db 7 RPR 9

RESULT 34
US-08-378-761A-68
; Sequence 68, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D

; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD
OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,761A
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-761A-68

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 NKK 5
|||
Db 2 NKK 4

RESULT 35
US-08-378-761A-70
; Sequence 70, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD
OF

; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,761A
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-761A-70

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NKK 5
|||
Db 4 NKK 6

RESULT 36
US-08-313-075A-12
; Sequence 12, Application US/08313075A
; Patent No. 5639870
; GENERAL INFORMATION:
; APPLICANT: Holton, Timothy A.
; APPLICANT: Cornish, Edwina C.
; APPLICANT: Tanaka, Yoshikazu
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
; TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City

STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,075A
FILING DATE: 30-NOV-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL 1538/92
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL 6698/93
FILING DATE: 07-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PCT/AU93/00127
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9433
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-313-075A-12

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
Db 5 GRR 7

RESULT 37
US-08-313-075A-14

; Sequence 14, Application US/08313075A
; Patent No. 5639870
; GENERAL INFORMATION:
; APPLICANT: Holton, Timothy A.
; APPLICANT: Cornish, Edwina C.
; APPLICANT: Tanaka, Yoshikazu
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
; TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR

;
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Scully, Scott, Murphy & Presser
;
; STREET: 400 Garden City Plaza
;
; CITY: Garden City
;
; STATE: New York
;
; COUNTRY: U.S.A.
;
; ZIP: 11530
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/313,075A
;
; FILING DATE: 30-NOV-1994
;
; CLASSIFICATION: 800
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: AU PL 1538/92
;
; FILING DATE: 27-MAR-1992
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: AU PL 6698/93
;
; FILING DATE: 07-JAN-1993
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: AU PCT/AU93/00127
;
; FILING DATE: 25-MAR-1993
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: DiGiglio, Frank S.
;
; REGISTRATION NUMBER: 31,346
;
; REFERENCE/DOCKET NUMBER: 9433
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (516) 742-4343
;
; TELEFAX: (516) 742-4366
;
; TELEX: 230 901 SANS UR
;
; INFORMATION FOR SEQ ID NO: 14:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 11 amino acids
;
; TYPE: amino acid
;
; STRANDEDNESS: single
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein

US-08-313-075A-14

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
 |||
Db 5 GRR 7

RESULT 38
US-08-485-286-68
;
; Sequence 68, Application US/08485286
;
; Patent No. 5646026
;
; Patent No. 5646026 5646119

; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD
OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,286
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378761
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-286-68

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NKK 5
|||
Db 2 NKK 4

RESULT 39
US-08-485-286-70
; Sequence 70, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119

; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD
OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,286
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378761
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-286-70

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NKK 5
|||
Db 4 NKK 6

RESULT 40
US-08-344-636-15
; Sequence 15, Application US/08344636
; Patent No. 5648336
; GENERAL INFORMATION:

; APPLICANT: STEWART, JOHN M.
; APPLICANT: GERA, LAJOS
; APPLICANT: WHALLEY, ERIC
; TITLE OF INVENTION: BRADYKININ ANTAGONIST PEPTIDES
; TITLE OF INVENTION: CONTAINING INDANE-SUBSTITUTED AMINO ACIDS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,636
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 216471/DKT. 19
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-344-636-15

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 2 RRP 4

RESULT 41
US-08-344-636-18
; Sequence 18, Application US/08344636
; Patent No. 5648336
; GENERAL INFORMATION:
; APPLICANT: STEWART, JOHN M.
; APPLICANT: GERA, LAJOS
; APPLICANT: WHALLEY, ERIC
; TITLE OF INVENTION: BRADYKININ ANTAGONIST PEPTIDES

; TITLE OF INVENTION: CONTAINING INDANE-SUBSTITUTED AMINO ACIDS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,636
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 216471/DKT. 19
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-344-636-18

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 2 RRP 4

RESULT 42
US-08-256-771-32
; Sequence 32, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; TITLE OF INVENTION: PRODUCTS THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington

STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys at position 10 is linked to
OTHER INFORMATION: Cys at position 35 of SEQ ID No. 5656591 10 by
disulfide bond"
US-08-256-771-32

```

Query Match           27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 3.1e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy          7 GRR 9
           |||
Db          1 GRR 3

```

RESULT 43
US-08-396-866-6
; Sequence 6, Application US/08396866
; Patent No. 5661124
; GENERAL INFORMATION:
; APPLICANT: Hoffman, Stephen J.
; APPLICANT: Nagai, Kiyoshi
; TITLE OF INVENTION: Blood Substitutes
; NUMBER OF SEQUENCES: 34

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 5797 Central Avenue
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.0.1
; SOFTWARE: Microsoft Word 5.0a
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/396,866
;
; FILING DATE:
; CLASSIFICATION: 530
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/062,780
;
; FILING DATE: May 17, 1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5661124ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: Hoffman
; REFERENCE/DOCKET NUMBER: 2A/CONT1
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-541-3322
;
; TELEFAX: 303-444-3013
;
; INFORMATION FOR SEQ ID NO: 6:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
;
; TYPE: amino acid
;
; TOPOLOGY: unknown to applicant
;
; MOLECULE TYPE: peptide
;
; HYPOTHETICAL: no
US-08-396-866-6

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
 |||
Db 5 GRR 7

RESULT 44
US-08-336-343A-24
;
; Sequence 24, Application US/08336343A
;
; Patent No. 5677144
;
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Alves, Frauke
;
; TITLE OF INVENTION: CCK-2, A No. 5677144el Receptor Tyrosine Kinase
;
; NUMBER OF SEQUENCES: 43
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
;
; STREET: 1155 Avenue of the Americas
;
; CITY: New York

STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,343A
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-065
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide

US-08-336-343A-24

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
Db 1 RPR 3

RESULT 45

US-08-469-582-7

; Sequence 7, Application US/08469582

; Patent No. 5677276

GENERAL INFORMATION:

APPLICANT: Dickerson, Kenneth T.

APPLICANT: Glass, James R.

APPPLICANT: Liu, Lin-Shu

APPLICANT: Polarek, James W.

APPLICANT: Craig, William S.

APPLICANT: Mullen, Daniel G.

APPLICANT: Cheng, Soan

TITLE OF INVENTION: Imm

TITLE OF INVENTION: Hyaluronate

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell

STREET: 4370 La J

CITY: San Diego

STATE: California

; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,582
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/363,213
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1550
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "Peptide is amidated at
; OTHER INFORMATION: C-terminus."
US-08-469-582-7

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GRR 9
|||
Db 1 GRR 3

RESULT 46
US-08-469-582-19
; Sequence 19, Application US/08469582
; Patent No. 5677276
; GENERAL INFORMATION:
; APPLICANT: Dickerson, Kenneth T.
; APPLICANT: Glass, James R.
; APPLICANT: Liu, Lin-Shu
; APPLICANT: Polarek, James W.
; APPLICANT: Craig, William S.
; APPLICANT: Mullen, Daniel G.
; APPLICANT: Cheng, Soan
; TITLE OF INVENTION: Immobilization of Peptides to
; TITLE OF INVENTION: Hyaluronate
; NUMBER OF SEQUENCES: 31

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,582
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 530
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/363,213
; FILING DATE: 23-DEC-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1550
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
;
; INFORMATION FOR SEQ ID NO: 19:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "Peptide is amidated at
; OTHER INFORMATION: C-terminus."
US-08-469-582-19

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
|||
Db 1 GRR 3

RESULT 47
US-08-479-400-4
;
; Sequence 4, Application US/08479400
; Patent No. 5679784
;
; GENERAL INFORMATION:
; APPLICANT: Ladant, Daniel
; APPLICANT: Leclerc, Claude
; APPLICANT: Sebo, Peter
; APPLICANT: Ullmann, Agnes
;
; TITLE OF INVENTION: Recombinant Mutants for Inducing

; TITLE OF INVENTION: Specific Immune Responses
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,400
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/011,644
; FILING DATE: 29-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495-0109-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-479-400-4

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TNK 4
|||
Db 7 TNK 9

RESULT 48
US-08-687-226-35
; Sequence 35, Application US/08687226
; Patent No. 5686068
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.; Visseren, M. W.;
; APPLICANT: van der Burg, Sjoerd; van der Bruggen, Pierre;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Derived From
; TITLE OF INVENTION: MAGE-2, Cytolytic T Cells Specific To Complexes Of
; TITLE OF INVENTION: Peptides And HLA-A2 Molecules, And Uses Thereof

NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,226
FILING DATE: 25-JULY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/217,188
FILING DATE: 24-MARCH-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5686068man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5447
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-687-226-35

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KTG 7
|||
Db 4 KTG 6

RESULT 49
US-08-687-226-60
; Sequence 60, Application US/08687226
; Patent No. 5686068
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.; Visseren, M. W.;
; APPLICANT: van der Burg, Sjoerd; van der Bruggen, Pierre;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Derived From
; TITLE OF INVENTION: MAGE-2, Cytolytic T Cells Specific To Complexes Of
; TITLE OF INVENTION: Peptides And HLA-A2 Molecules, And Uses Thereof
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/687,226
FILING DATE: 25-JULY-1996
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/217,188
FILING DATE: 24-MARCH-1994

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5686068man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5447

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 60:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

```

Query Match           27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 3.1e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      5 KTG 7
       |||
Db      1 KTG 3

```

RESULT 50
US-08-687-226-67
; Sequence 67, Application US/08687226
; Patent No. 5686068
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.; Visseren, M. W.;
; APPLICANT: van der Burg, Sjoerd; van der Bruggen, Pierre;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Derived From
; TITLE OF INVENTION: MAGE-2, Cytolytic T Cells Specific To Complexes Of
; TITLE OF INVENTION: Peptides And HLA-A2 Molecules, And Uses Thereof
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue

CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,226
FILING DATE: 25-JULY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/217,188
FILING DATE: 24-MARCH-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5686068man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5447
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-687-226-67

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KTG 7
|||
Db 5 KTG 7

RESULT 51
US-08-615-181-88
; Sequence 88, Application US/08615181
; Patent No. 5756666
; GENERAL INFORMATION:
; APPLICANT: MASAFUMI, TAKIGUCHI
; APPLICANT: MIWA, KIYOSHI
; TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE
; TITLE OF INVENTION: RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND
; TITLE OF INVENTION: CURING AIDS
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA

; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,181
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/01756
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 261302/1993
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-796-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-08-615-181-88

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KTG 7
 |||
Db 7 KTG 9

RESULT 52
US-08-477-509B-36
; Sequence 36, Application US/08477509B
; Patent No. 5770697
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A
; APPLICANT: Cappello, Joseph
; APPLICANT: Crissman, John w
; APPLICANT: Dorman, Mary A
; TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the
Same
; NUMBER OF SEQUENCES: 112

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,509B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,155
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,049
; FILING DATE: 22-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/114,618
; FILING DATE: 29-OCT-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/927,258
; FILING DATE: 04-NOV-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-509B-36

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGR 8
|||
Db 3 TGR 5

RESULT 53
US-08-082-269D-5
; Sequence 5, Application US/08082269D
; Patent No. 5773227

; GENERAL INFORMATION:
; APPLICANT: Kuhn, Michael
; APPLICANT: Meyer, Tobias
; APPLICANT: Allbritton, Nancy
; TITLE OF INVENTION: Bifunctional Chelating Polysaccharides
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Molecular Probes, Inc.
; STREET: 4849 Pitchford Avenue
; CITY: Eugene
; STATE: Oregon
; COUNTRY: USA
; ZIP: 97402-9144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM
; OPERATING SYSTEM: MS-DOS 6.2
; SOFTWARE: Text Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,269D
; FILING DATE: 23-June-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Helfenstein, Allegra J.
; REGISTRATION NUMBER: 34,179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503)465-8300
; TELEFAX: (503)344-6504
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 AMINO ACIDS
; TYPE: Amino Acid
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; HYPOTHETICAL: no
; FRAGMENT TYPE:
; PUBLICATION INFORMATION:
; AUTHORS: Chelsky, Daniel, Ralph, Rebecca and Jonak, Gerald
; TITLE: Sequence Requirements for Synthetic Peptide-Mediated
Translocation to the
; Patent No. 5773227
; JOURNAL: Molecular and Cellular Biology
; VOLUME: 9
; ISSUE: 6
; PAGES: 2487-2492
; DATE: 1989
US-08-082-269D-5

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 RPR 11
Db 8 RPR 10

RESULT 54
US-08-082-269D-8
; Sequence 8, Application US/08082269D
; Patent No. 5773227
; GENERAL INFORMATION:
; APPLICANT: Kuhn, Michael
; APPLICANT: Meyer, Tobias
; APPLICANT: Allbritton, Nancy
; TITLE OF INVENTION: Bifunctional Chelating Polysaccharides
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Molecular Probes, Inc.
; STREET: 4849 Pitchford Avenue
; CITY: Eugene
; STATE: Oregon
; COUNTRY: USA
; ZIP: 97402-9144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM
; OPERATING SYSTEM: MS-DOS 6.2
; SOFTWARE: Text Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,269D
; FILING DATE: 23-June-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Helfenstein, Allegra J.
; REGISTRATION NUMBER: 34,179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503)465-8300
; TELEFAX: (503)344-6504
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 AMINO ACIDS
; TYPE: Amino Acid
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; HYPOTHETICAL: no
; FRAGMENT TYPE:
US-08-082-269D-8

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 8 RPR 10

RESULT 55
US-08-259-550A-5
; Sequence 5, Application US/08259550A
; Patent No. 5776892
; GENERAL INFORMATION:
; APPLICANT: Counts, David F.

; APPLICANT: Duff, Ronald G.
; TITLE OF INVENTION: Anti-Inflammatory Peptides
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,550A
; FILING DATE: 16-JUN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7142-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-259-550A-5

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 RPR 11
|||
Db 6 RPR 8

RESULT 56
US-08-290-301-34
; Sequence 34, Application US/08290301
; Patent No. 5792921
; GENERAL INFORMATION:
; APPLICANT: Londesborough, John
; APPLICANT: Tunnela, Outi
; APPLICANT: Palva, Tupio
; APPLICANT: Holmstrom, Kjell-Ove
; APPLICANT: Welin, Bjorn
; APPLICANT: Mandel, Abul

; TITLE OF INVENTION: Increasing the trehalose content
; TITLE OF INVENTION: of organisms by transforming them with combinations of
; TITLE OF INVENTION: the structural genes for trehalose synthase.
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Alko Ltd.
; STREET: PO Box 350
; CITY: Helsinki
; STATE: -
; COUNTRY: Finland
; ZIP: SF-00101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WP5.1 file exported as DOS text file
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,301
; FILING DATE: 15 August 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FI 943133
; FILING DATE: 29 June 1994
; APPLICATION NUMBER: PCT/FI93/00049
; FILING DATE: 15 February 1993
; APPLICATION NUMBER: 07/841,997
; FILING DATE: 28 February 1992
; APPLICATION NUMBER: 07/836,021
; FILING DATE: 14 February 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubovcik, Ronald J.
; NAME: Lydon, James C.
; REGISTRATION NUMBER: 25,401
; REGISTRATION NUMBER: 30,082
; REFERENCE/DOCKET NUMBER: LAIN-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 467-6300
; TELEFAX: (202) 466-2006
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: Amino acid
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; HYPOTHETICAL: No
; FRAGMENT TYPE: N-terminal
US-08-290-301-34

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TNK 4
|||
Db 9 TNK 11

RESULT 57

US-08-381-984-32

; Sequence 32, Application US/08381984

; Patent No. 5804555

; GENERAL INFORMATION:

; APPLICANT: Mamoru TOMITA et al.

; TITLE OF INVENTION: ANTIOXIDANT

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/381,984

; FILING DATE: April 11, 1995

; CLASSIFICATION: 252

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Warren M. Cheek, Jr.

; REGISTRATION NUMBER: 33,367

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-8850

; TELEFAX:

; TELEX:

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY:

; LOCATION:

; IDENTIFICATION METHOD:

; OTHER INFORMATION: /note= "the specified peptide as well as

; OTHER INFORMATION: peptides including the specified peptide as a
fragment thereof"

; FEATURE:

; NAME/KEY:

; LOCATION:

; IDENTIFICATION METHOD:

; OTHER INFORMATION: /note= "cysteine residues at position 10

; OTHER INFORMATION: is linked by disulfide linkage with the cysteine
residue at pos

; OTHER INFORMATION: SEQ ID No. 5804555 29"

US-08-381-984-32

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
|||
Db 1 GRR 3

RESULT 58

US-08-669-721-17

; Sequence 17, Application US/08669721
; Patent No. 5834236
; GENERAL INFORMATION:
; APPLICANT: Lamb et al., Christopher J.
; TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND
; TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,721
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellison, Eldora L.
; REGISTRATION NUMBER: 39,967
; REFERENCE/DOCKET NUMBER: 07251/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-669-721-17

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10

|||
Db 4 RRP 6

RESULT 59
US-08-669-721-18
; Sequence 18, Application US/08669721
; Patent No. 5834236
; GENERAL INFORMATION:
; APPLICANT: Lamb et al., Christopher J.
; TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND
; TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,721
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellison, Eldora L.
; REGISTRATION NUMBER: 39,967
; REFERENCE/DOCKET NUMBER: 07251/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-669-721-18

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 4 RRP 6

RESULT 60
US-08-669-721-19
; Sequence 19, Application US/08669721

; Patent No. 5834236
; GENERAL INFORMATION:
; APPLICANT: Lamb et al., Christopher J.
; TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND
; TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,721
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellison, Eldora L.
; REGISTRATION NUMBER: 39,967
; REFERENCE/DOCKET NUMBER: 07251/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-669-721-19

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
|||
Db 4 GRR 6

RESULT 61
US-08-669-721-20
; Sequence 20, Application US/08669721
; Patent No. 5834236
; GENERAL INFORMATION:
; APPLICANT: Lamb et al., Christopher J.
; TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND
; TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:

;
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,721
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 435
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellison, Eldora L.
; REGISTRATION NUMBER: 39,967
; REFERENCE/DOCKET NUMBER: 07251/014001
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
;
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-669-721-20

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
 |||
Db 4 GRR 6

RESULT 62
US-08-508-664-13
;
; Sequence 13, Application US/08508664
; Patent No. 5840542
;
; GENERAL INFORMATION:
; APPLICANT: KANG, Yup
; APPLICANT: YOON, Ji-Won
; TITLE OF INVENTION: METHOD FOR MANUFACTURE OF PROINSULIN
; TITLE OF INVENTION: WITH HIGH EXPORT YIELD
; NUMBER OF SEQUENCES: 25
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/508,664
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, S. Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0136/0B300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CONN PEPTIDE

US-08-508-664-13

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KTG 7
 |||
Db 6 KTG 8

RESULT 63

US-08-701-124-19

; Sequence 19, Application US/08701124

; Patent No. 5846782

; GENERAL INFORMATION:

; APPLICANT: Wickham, Thomas J.

; APPLICANT: Roelvink, Petrus W.

; APPLICANT: Kovacs, Imre

; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF

; TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS

; NUMBER OF SEQUENCES: 80

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Leydig, Voit & Mayer, Ltd.

; STREET: Two Prudential Plaza - 49th Floor

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60601

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/701,124
; FILING DATE: 21-AUG-1996
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-701-124-19

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKT 6
|||
Db 8 KKT 10

RESULT 64
US-08-473-025-12
; Sequence 12, Application US/08473025
; Patent No. 5851994
; GENERAL INFORMATION:
; APPLICANT: Schreiber, Ronda
; APPLICANT: Polarek, James
; TITLE OF INVENTION: Compositions that Inhibit Wound
; TITLE OF INVENTION: Contraction and Methods of Using Same
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,025
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/234,979
; FILING DATE: 28-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-LA 1597
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-473-025-12

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
|||
Db 1 GRR 3

RESULT 65

US-08-502-046-2

; Sequence 2, Application US/08502046
; Patent No. 5861487
; GENERAL INFORMATION:
; APPLICANT: Holton, Timothy A.
; APPLICANT: Cornish, Edwina C.
; APPLICANT: Kovacic, Filippa
; APPLICANT: Tanaka, Yoshikazu
; APPLICANT: Lester, Diane R.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
; TITLE OF INVENTION: HYDROXYLASE AND USES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/502,046
; FILING DATE: 14-JUL-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/285,309
; FILING DATE: 03-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8633Z
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-502-046-2

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
|||
Db 5 GRR 7

RESULT 66

US-08-502-046-13

; Sequence 13, Application US/08502046

; Patent No. 5861487

; GENERAL INFORMATION:

; APPLICANT: Holton, Timothy A.

; APPLICANT: Cornish, Edwina C.

; APPLICANT: Kovacic, Filippa

; APPLICANT: Tanaka, Yoshikazu

; APPLICANT: Lester, Diane R.

; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-

; TITLE OF INVENTION: HYDROXYLASE AND USES

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Scully, Scott, Murphy & Presser

; STREET: 400 Garden City Plaza

; CITY: Garden City

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 11530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/502,046

; FILING DATE: 14-JUL-1995

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/285,309

; FILING DATE: 03-AUG-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: DiGiglio, Frank S.

; REGISTRATION NUMBER: 31,346

; REFERENCE/DOCKET NUMBER: 8633Z

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-502-046-13

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GRR 9
|||
Db 5 GRR 7

RESULT 67
US-08-502-046-15
; Sequence 15, Application US/08502046
; Patent No. 5861487
; GENERAL INFORMATION:
; APPLICANT: Holton, Timothy A.
; APPLICANT: Cornish, Edwina C.
; APPLICANT: Kovacic, Filipa
; APPLICANT: Tanaka, Yoshikazu
; APPLICANT: Lester, Diane R.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
; TITLE OF INVENTION: HYDROXYLASE AND USES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/502,046
; FILING DATE: 14-JUL-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/285,309
; FILING DATE: 03-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346

; REFERENCE/DOCKET NUMBER: 8633Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

US-08-502-046-15

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
 |||
Db 5 GRR 7

RESULT 68

US-08-633-148-6

; Sequence 6, Application US/08633148
; Patent No. 5864018
; GENERAL INFORMATION:
; APPLICANT: MORSER, MICHAEL J.
; APPLICANT: NAGASHIMA, MARIKO
; APPLICANT: HOLLANDER, DORIS A.
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,148
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY ESQ., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 014618-005600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-633-148-6

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGR 8
|||
Db 5 TGR 7

RESULT 69

US-08-397-286-4

; Sequence 4, Application US/08397286

; Patent No. 5871747

; GENERAL INFORMATION:

; APPLICANT: GENGOUX, CHRISTINE; LeCLERC, CLAUDE

; TITLE OF INVENTION: ANTIGEN-CARRYING

; TITLE OF INVENTION: MICROPARTICLES AND THEIR USE IN THE IN THE

; TITLE OF INVENTION: INDUCTION OF HUMORAL OR CELLULAR RESPONSES

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIERMAN & MUSERLIAN

; STREET: 600 THIRD AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: U.S.A.

; ZIP: 10016

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASC II

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/397,286

; FILING DATE: 10-MAR-1995

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/FR93/00876

; FILING DATE: 13-SEP-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR/92/10879

; FILING DATE: 11-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: CHARLES A. MUSERLIAN

; REGISTRATION NUMBER: 19,683

; REFERENCE/DOCKET NUMBER: 102.162

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-661-8000

; TELEFAX: 212-661-8002

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: AMINO ACID
; STRANDEDNESS: UNKNOWN
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE: PEPTIDE
US-08-397-286-4

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TNK 4
|||
Db 7 TNK 9

RESULT 70

US-08-428-257A-54

; Sequence 54, Application US/08428257A

; Patent No. 5885808

; GENERAL INFORMATION:

; APPLICANT: Spooner, Robert A.

; APPLICANT: Epenetos, A.A.

; TITLE OF INVENTION: Compounds to target cells

; NUMBER OF SEQUENCES: 80

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jules E. Goldberg

; STREET: 261 Madison Avenue

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10016-2391

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/428,257A

; FILING DATE: 07/05/95

; CLASSIFICATION: 514

; INFORMATION FOR SEQ ID NO: 54:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-428-257A-54

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKT 6
|||

Db

3 KKT 5

RESULT 71
US-08-934-222-77
; Sequence 77, Application US/08934222
; Patent No. 5928896
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,222
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-934-222-77

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10

|||

Db 3 RRP 5

RESULT 72

US-08-395-204-4

; Sequence 4, Application US/08395204

; Patent No. 5935580

; GENERAL INFORMATION:

; APPLICANT: Ladant, Daniel

; APPLICANT: Leclerc, Claude

; APPLICANT: Sebo, Peter

; APPLICANT: Ullmann, Agnes

; TITLE OF INVENTION: Recombinant Mutants for Inducing

; TITLE OF INVENTION: Specific Immune Responses

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/395,204

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/871,795

; FILING DATE: 21-APR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Kenneth J.

; REGISTRATION NUMBER: 25,146

; REFERENCE/DOCKET NUMBER: 03495-0109-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-408-4000

; TELEFAX: 202-408-4400

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-395-204-4

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TNK 4

|||

Db 7 TNK 9

RESULT 73
US-08-933-402-77
; Sequence 77, Application US/08933402
; Patent No. 5948887
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,402
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-933-402-77

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
 |||
Db 3 RRP 5

RESULT 74

US-09-207-621-77

; Sequence 77, Application US/09207621

; Patent No. 5952465

; GENERAL INFORMATION:

; APPLICANT: EVANS, Herbert J.

; APPLICANT: KINI, R. Manjunatha

; TITLE OF INVENTION: Polypeptides That Include Conformation-

; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction Sit

; NUMBER OF SEQUENCES: 153

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: Suite 500, 3000 K Street NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/207,621

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/532,818

; FILING DATE: 03-MAY-1996

; APPLICATION NUMBER: PCT/US94/04294

; FILING DATE: 21-APR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/143,364

; FILING DATE: 29-OCT-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/051,741

; FILING DATE: 23-APR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Isaacson, John P.

; REGISTRATION NUMBER: 33,751

; REFERENCE/DOCKET NUMBER: 040433/0148

; INFORMATION FOR SEQ ID NO: 77:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-09-207-621-77

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10

|||

Db 3 RRP 5

RESULT 75
US-08-645-193B-55
; Sequence 55, Application US/08645193B
; Patent No. 5962253
; GENERAL INFORMATION:
; APPLICANT: Kupke, Thomas
; APPLICANT: Gotz, Friedrich
; APPLICANT: Kempfer, Christoph
; APPLICANT: Jung, Gunther
; TITLE OF INVENTION: Oxidative Decarboxylation of Peptides
; TITLE OF INVENTION: Catalyzed by Flavoprotein EpiD
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,193B
; FILING DATE: 13-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0652.1540000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-645-193B-55

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KTG 7
|||
Db 2 KTG 4

Search completed: April 8, 2004, 15:52:09
Job time : 12.3077 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 8.61538 Seconds
(without alignments)
122.816 Million cell updates/sec

Title: US-09-787-443A-9

Perfect score: 11

Sequence: 1 ATNKKTGRRPR 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 226

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : PIR_78:*

1: pirl:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	3	27.3	11	2	JN0023	substance P - chic
2	3	27.3	11	2	PD0441	translation elonga
3	3	27.3	11	4	I54081	retinoic acid rece
4	2	18.2	11	1	XAVIBH	bradykinin-potenti
5	2	18.2	11	1	XASNBA	bradykinin-potenti
6	2	18.2	11	1	SPHO	substance P - hors
7	2	18.2	11	1	A60654	substance P - guin
8	2	18.2	11	2	S32575	ribosomal protein
9	2	18.2	11	2	PQ0682	photosystem I 17.5
10	2	18.2	11	2	A26930	ermG leader peptid
11	2	18.2	11	2	A61365	phyllokinin - Rohd
12	2	18.2	11	2	B26744	megascoliakinin -
13	2	18.2	11	2	S23308	substance P - rain

14	2	18.2	11	2	S23306	substance P - Atla
15	2	18.2	11	2	S07201	physalaemin - frog
16	2	18.2	11	2	S42449	ant1 protein - pha
17	2	18.2	11	2	A58502	38K kidney stone p
18	2	18.2	11	2	JQ0395	hypothetical prote
19	2	18.2	11	2	S66606	quinoline 2-oxidor
20	2	18.2	11	2	I41138	acetyl ornithine d
21	2	18.2	11	2	S42587	celf protein - Esc
22	2	18.2	11	2	S33782	acetolactate synth
23	2	18.2	11	2	B41835	translation elonga
24	2	18.2	11	2	S14087	parasporal crystal
25	2	18.2	11	2	A44755	20alpha-hydroxyste
26	2	18.2	11	2	E41476	probable antigen 5
27	2	18.2	11	2	S33519	probable secreted
28	2	18.2	11	2	S19775	wound-induced prot
29	2	18.2	11	2	PC4267	ribosomal protein
30	2	18.2	11	2	PQ0731	unidentified 5.7/3
31	2	18.2	11	2	PC2173	triacylglycerol li
32	2	18.2	11	2	S78026	ribosomal protein
33	2	18.2	11	2	A34135	DNA-binding protei
34	2	18.2	11	2	A61512	variant surface gl
35	2	18.2	11	2	A26120	6-phosphofructokin
36	2	18.2	11	2	A34662	Achatina cardio-ex
37	2	18.2	11	2	S05002	corazonin - Americ
38	2	18.2	11	2	S33300	probable substance
39	2	18.2	11	2	C37196	bradykinin-potenti
40	2	18.2	11	2	D37196	bradykinin-potenti
41	2	18.2	11	2	D57789	gallbladder stone
42	2	18.2	11	2	PT0250	Ig heavy chain CRD
43	2	18.2	11	2	PT0273	Ig heavy chain CRD
44	2	18.2	11	2	PT0287	Ig heavy chain CRD
45	2	18.2	11	2	PT0302	Ig heavy chain CRD
46	2	18.2	11	2	S13279	Ile-Ser-bradykinin
47	2	18.2	11	2	I54193	Rhesus blood group
48	2	18.2	11	2	S51732	T-cell receptor al
49	2	18.2	11	2	S23926	major glycoprotein
50	2	18.2	11	2	S54347	tubulin beta chain
51	2	18.2	11	2	A14454	6-phosphofructokin
52	2	18.2	11	2	B29806	acidic proline-ric
53	2	18.2	11	2	A29806	acidic proline-ric
54	2	18.2	11	2	PH1632	Ig H chain V-D-J r
55	2	18.2	11	2	PH1376	T antigen variant
56	2	18.2	11	2	PT0211	T-cell receptor al
57	2	18.2	11	2	C38887	T-cell receptor ga
58	2	18.2	11	2	S45386	low density lipopr
59	2	18.2	11	2	S09349	microtubule-associ
60	2	18.2	11	2	PH0929	T-cell receptor be
61	2	18.2	11	2	PH0938	T-cell receptor be
62	2	18.2	11	2	PH0947	T-cell receptor be
63	2	18.2	11	2	PH0919	T-cell receptor be
64	2	18.2	11	2	I52304	gene rSSTR4 protei
65	2	18.2	11	2	A48973	glucoamylase A1 (E
66	2	18.2	11	2	PN0169	NADH2 dehydrogenas
67	2	18.2	11	4	S52252	hypothetical prote
68	2	18.2	11	4	S19015	hypothetical prote
69	1	9.1	11	1	ECLQ2M	tachykinin II - mi
70	1	9.1	11	1	EOOCC	eledoisin - curled

71	1	9.1	11	1	EOOC	eleodoisin - musky
72	1	9.1	11	1	GMROL	leucosulfakinin -
73	1	9.1	11	1	LFTWWE	probable trpEG lea
74	1	9.1	11	2	S66196	alcohol dehydrogen
75	1	9.1	11	2	G42762	proteasome endopep
76	1	9.1	11	2	S68392	H+-transporting tw
77	1	9.1	11	2	A33917	dihydroorotate (EC
78	1	9.1	11	2	B49164	chromogranin-B - r
79	1	9.1	11	2	A40693	transgelin - sheep
80	1	9.1	11	2	A38841	rhodopsin homolog
81	1	9.1	11	2	S00616	parasporal crystal
82	1	9.1	11	2	C53652	rh1R protein - Pse
83	1	9.1	11	2	S09074	cytochrome P450-4b
84	1	9.1	11	2	A57458	gene Gax protein -
85	1	9.1	11	2	D60409	kassinin-like pept
86	1	9.1	11	2	F60409	substance P-like p
87	1	9.1	11	2	E60409	substance P-like p
88	1	9.1	11	2	YHRT	morphogenetic neur
89	1	9.1	11	2	YHHU	morphogenetic neur
90	1	9.1	11	2	YHBO	morphogenetic neur
91	1	9.1	11	2	YHXAE	morphogenetic neur
92	1	9.1	11	2	YHJFHY	morphogenetic neur
93	1	9.1	11	2	B60409	kassinin-like pept
94	1	9.1	11	2	C60409	kassinin-like pept
95	1	9.1	11	2	S07203	uperolein - frog (
96	1	9.1	11	2	S07207.	Crinia-angiotensin
97	1	9.1	11	2	A61033	ranatachykinin A -
98	1	9.1	11	2	D61033	ranatachykinin D -
99	1	9.1	11	2	B58501	24K kidney and bla
100	1	9.1	11	2	D58502	27K bile and gallb

ALIGNMENTS

RESULT 1

JN0023

substance P - chicken

C;Species: Gallus gallus (chicken)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jul-1997

C;Accession: JN0023

R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.

Regul. Pept. 20, 171-180, 1988

A;Title: [Arg3]substance P and neuropeptide A from chicken small intestine.

A;Reference number: JN0023; MUID:88204263; PMID:2452461

A;Accession: JN0023

A;Molecule type: protein

A;Residues: 1-11 <CON>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11

|||
Db 1 RPR 3

RESULT 2

PD0441

translation elongation factor TU-like protein P43, mitochondrial - mouse
(fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 21-Aug-1998
C;Accession: PD0441
R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.
submitted to JIPID, August 1998
A;Description: Proteome analysis of mouse brain.
A;Reference number: PD0441
A;Accession: PD0441
A;Molecule type: protein
A;Residues: 1-11 <KAW>
A;Experimental source: striatum
C;Keywords: mitochondrion

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKT 6
|||
Db 5 KKT 7

RESULT 3

I54081

retinoic acid receptor alpha, exon 3 (mistranslated) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999
C;Accession: I54081
R;Dong, S.; Geng, J.P.; Tong, J.H.; Wu, Y.; Cai, J.R.; Sun, G.L.; Chen, S.R.;
Wang, Z.Y.; Larsen, C.J.; Berger, R.
Genes Chromosomes Cancer 6, 133-139, 1993
A;Title: Breakpoint clusters of the PML gene in acute promyelocytic leukemia:
primary structure of the reciprocal products of the PML-RARA gene in a patient
with t(15;17).
A;Reference number: I54081; MUID:93222087; PMID:7682097
A;Accession: I54081
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-11 <DON>
A;Cross-references: GB:S57794; NID:g299073; PIDN:AAD13888.1; PID:g4261588
A;Note: the translation is from an incorrect reading frame
C;Genetics:
A;Gene: GDB:RARA
A;Cross-references: GDB:120337; OMIM:180240
A;Map position: 17q12-17q12

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 3 RPR 5

RESULT 4
XAVIBH
bradykinin-potentiating peptide - halys viper
N;Alternate names: BPP
C;Species: Agkistrodon halys (halys viper)
C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 05-Aug-1994
C;Accession: JC0002
R;Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.
Peptides 6, 339-342, 1985
A;Title: Structure-function studies on the bradykinin potentiating peptide from
Chinese snake venom (Agkistrodon halys Pallas).
A;Reference number: JC0002; MUID:86177022; PMID:3008123
A;Accession: JC0002
A;Molecule type: protein
A;Residues: 1-11 <CHI>
C;Comment: Because this peptide both inhibits the activity of the angiotensin-
converting enzyme and enhances the action of bradykinin, it is an
antihypertensive agent.
C;Superfamily: bradykinin-potentiating peptide
C;Keywords: angiotensin-converting enzyme inhibitor; antihypertensive;
bradykinin; pyroglutamic acid; venom
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GR 8
|||
Db 2 GR 3

RESULT 5
XASNBA
bradykinin-potentiating peptide B - mamushi
C;Species: Agkistrodon blomhoffi (mamushi)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995
C;Accession: A01254
R;Kato, H.; Suzuki, T.
Proc. Jpn. Acad. 46, 176-181, 1970
A;Reference number: A01254
A;Accession: A01254
A;Molecule type: protein
A;Residues: 1-11 <KAT>
A;Note: the sequence of the natural peptide was confirmed by the synthesis and
analysis of a peptide having the identical structure and biological properties
C;Superfamily: bradykinin-potentiating peptide
C;Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic
acid; venom
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 5 PR 6

RESULT 6

SPHO

substance P - horse

C;Species: Equus caballus (domestic horse)

C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 23-Aug-1996

C;Accession: A01558

R;Studer, R.O.; Trzeciak, A.; Lergier, W.

Helv. Chim. Acta 56, 860-866, 1973

A;Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pferdedarm.

A;Reference number: A01558

A;Accession: A01558

A;Molecule type: protein

A;Residues: 1-11 <STU>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RP 10
||
Db 1 RP 2

RESULT 7

A60654

substance P - guinea pig

C;Species: Cavia porcellus (guinea pig)

C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 08-Dec-1995

C;Accession: A60654

R;Murphy, R.

Neuropeptides 14, 105-110, 1989

A;Title: Primary amino acid sequence of guinea-pig substance P.

A;Reference number: A60654; MUID:90044685; PMID:2478925

A;Accession: A60654

A;Molecule type: protein

A;Residues: 1-11 <MUR>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RP 10

||
Db 1 RP 2

RESULT 8

S32575

ribosomal protein S2, plastid - squawroot plastid (fragment)
C;Species: plastid *Conopholis americana* (squawroot)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 13-Aug-1999
C;Accession: S32575
R;Taylor, G.W.; Wolfe, K.H.; Morden, C.W.; dePamphilis, C.W.; Palmer, J.D.
Curr. Genet. 20, 515-518, 1991
A;Title: Lack of a functional plastid tRNA(Cys) gene is associated with loss of
photosynthesis in a lineage of parasitic plants.
A;Reference number: S32575; MUID:92145776; PMID:1723664
A;Accession: S32575
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-11 <TAY>
A;Cross-references: EMBL:X64567; NID:g11275; PIDN:CAA45868.1; PID:g11276
C;Genetics:
A;Gene: rps2
A;Genome: plastid
C;Superfamily: *Escherichia coli* ribosomal protein S2
C;Keywords: plastid; protein biosynthesis; ribosome

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RR 9
||
Db 3 RR 4

RESULT 9

PQ0682

photosystem I 17.5K D2 chain - common tobacco (fragment)
C;Species: *Nicotiana tabacum* (common tobacco)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C;Accession: PQ0682
R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.
Plant Physiol. 102, 1259-1267, 1993
A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH and
psaL are all present in isoforms in *Nicotiana* spp.
A;Reference number: PQ0667; MUID:94105345; PMID:8278548
A;Accession: PQ0682
A;Molecule type: protein
A;Residues: 1-11 <OBO>
C;Superfamily: photosystem I chain II
C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AT 2

||
Db 5 AT 6

RESULT 10
A26930
ermG leader peptide 1 - *Bacillus sphaericus*
C;Species: *Bacillus sphaericus*
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 24-Sep-1999
C;Accession: A26930
R;Monod, M.; Mohan, S.; Dubnau, D.
J. Bacteriol. 169, 340-350, 1987
A;Title: Cloning and analysis of ermG, a new macrolide-lincosamide-streptogramin
B resistance element from *Bacillus sphaericus*.
A;Reference number: A91840; MUID:87083389; PMID:3025178
A;Accession: A26930
A;Molecule type: DNA
A;Residues: 1-11 <MON>
A;Cross-references: GB:M15332; NID:g142881; PIDN:AAA22417.1; PID:g142882
C;Superfamily: unassigned leader peptides

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NK 4
||
Db 2 NK 3

RESULT 11
A61365
phyllokinin - Rohde's leaf frog
N;Alternate names: bradykinyl-isoleucyl-tyrosine O-sulfate
C;Species: *Phylomedusa rohdei* (Rohde's leaf frog)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000
C;Accession: A61365
R;Anastasi, A.; Bertaccini, G.; Erspamer, V.
Br. J. Pharmacol. 27, 479-485, 1966
A;Title: Pharmacological data on phyllokinin (bradykinyl-isoleucyl-tyrosine O-
sulphate) and bradykinyl-isoleucyl-tyrosine.
A;Reference number: A61365; MUID:67179312; PMID:5970899
A;Accession: A61365
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <ANA>
C;Superfamily: unassigned animal peptides
C;Keywords: sulfoprotein
F;11/Binding site: sulfate (Tyr) (covalent) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RP 10
||
Db 1 RP 2

RESULT 12

B26744

megascoliakinin - garden dagger wasp

N;Alternate names: 6-Thr-bradykinin-Lys-Ala

C;Species: Megascolia flavifrons (garden dagger wasp)

C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 18-Aug-2000

C;Accession: B26744; A28609

R;Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.

Toxicon 25, 527-535, 1987

A;Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp Megascolia flavifrons.

A;Reference number: A94322; MUID:87293024; PMID:3617088

A;Accession: B26744

A;Molecule type: protein

A;Residues: 1-11 <YAS>

R;Nakajima, T.; Piek, T.; Yashuara, T.; Mantel, P.

Toxicon 26, 34, 1988

A;Title: Two kinins isolated from the venom of Megascolia flavifrons.

A;Reference number: A28609

A;Accession: A28609

A;Molecule type: protein

A;Residues: 1-11 <NAK>

C;Superfamily: unassigned animal peptides

C;Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.08; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RP 10
||
Db 1 RP 2

RESULT 13

S23308

substance P - rainbow trout

C;Species: Oncorhynchus mykiss (rainbow trout)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000

C;Accession: S23308

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neuropeptide-A-related peptides from the brain of the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23308

A;Molecule type: protein

A;Residues: 1-11 <JEN>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Superfamily: unassigned animal peptides

C;Keywords: neuropeptide; amidated carboxyl end; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 PR 11
||
Db 2 PR 3

RESULT 14

S23306

substance P - Atlantic cod

C;Species: *Gadus morhua* (Atlantic cod)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000

C;Accession: S23306

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neuropeptide-A-related peptides from the brain of the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23306

A;Molecule type: protein

A;Residues: 1-11 <JEN>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Superfamily: unassigned animal peptides

C;Keywords: neuropeptide; amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 PR 11
||
Db 2 PR 3

RESULT 15

S07201

physalaemin - frog (*Physalaemus fuscomaculatus*)

C;Species: *Physalaemus fuscomaculatus*

C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000

C;Accession: S07201

R;Erspamer, V.; Anastasi, A.; Bertaccini, G.; Cei, J.M.

Experientia 20, 489-490, 1964

A;Title: Structure and pharmacological actions of physalaemin, the main active polypeptide of the skin of *Physalaemus fuscomaculatus*.

A;Reference number: S07201; MUID:66076612; PMID:5857249

A;Accession: S07201

A;Molecule type: protein
A;Residues: 1-11 <ERS>
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NK 4
||
Db 5 NK 6

RESULT 16
S42449
anti protein - phage P7
C;Species: phage P7
C;Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 08-Oct-1999
C;Accession: S42449
R;Citron, M.; Schuster, H.
Cell 62, 591-598, 1990
A;Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.
A;Reference number: S42448; MUID:90335968; PMID:1696181
A;Accession: S42449
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-11 <CIT>
A;Cross-references: EMBL:M35139; NID:g215705; PIDN:AAA32437.1; PID:g215707

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KK 5
||
Db 2 KK 3

RESULT 17
A58502
38K kidney stone protein - unidentified bacterium (fragment)
C;Species: unidentified bacterium
C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C;Accession: A58502
R;Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A;Description: The proteins of kidney and gallbladder stones.
A;Reference number: A58501
A;Accession: A58502
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <BIN>
A;Experimental source: human kidney stone containing Ca ox.mono and dihyd, 1%
struvite, CaPO4 carbonate & hydrox., and 4% protein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TG 7
||
Db 4 TG 5

RESULT 18

JQ0395

hypothetical protein (nodB 3' region) - Azorhizobium caulinodans
N;Alternate names: hypothetical 1.4K protein
C;Species: Azorhizobium caulinodans
A;Note: host Sesbania rostrata
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 03-Feb-1994
C;Accession: JQ0395
R;Goethals, K.; Gao, M.; Tomekpe, K.; Van Montagu, M.; Holsters, M.
Mol. Genet. 219, 289-298, 1989
A;Title: Common nodABC genes in Nod locus 1 of Azorhizobium caulinodans:
nucleotide sequence and plant-inducible expression.
A;Reference number: JQ0393; MUID:90136519; PMID:2615763
A;Accession: JQ0395
A;Molecule type: DNA
A;Residues: 1-11 <GOE>
A;Cross-references: GB:L18897
A;Experimental source: strain ORS571

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RR 9
||
Db 2 RR 3

RESULT 19

S66606

quinoline 2-oxidoreductase alpha chain - Comamonas testosteroni (fragment)
C;Species: Comamonas testosteroni
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S66606
R;Schach, S.; Tshisuaka, B.; Fetzner, S.; Lingens, F.
Eur. J. Biochem. 232, 536-544, 1995
A;Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from Comamonas testosteroni 63. The first two enzymes in quinoline and 3-methylquinoline degradation.
A;Reference number: S66606; MUID:96035889; PMID:7556204
A;Accession: S66606
A;Molecule type: protein
A;Residues: 1-11 <SCH>
A;Experimental source: strain 63

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 PR 11
||
Db 10 PR 11

RESULT 20
I41138
acetyl ornithine deacetylase (argE) - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 08-Oct-1999
C;Accession: I41138
R;Charlier, D.; Piette, J.; Glansdorff, N.
Nucleic Acids Res. 10, 5935-5948, 1982
A;Title: is3 can function as a mobile promoter in e.coli.
A;Reference number: I41137; MUID:83064529; PMID:6292860
A;Accession: I41138
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-11 <RES>
A;Cross-references: GB:J01589; NID:g145346; PIDN:AAA23485.1; PID:g551788

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 TG 7
||
Db 9 TG 10

RESULT 21
S42587
celF protein - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C;Accession: S42587
R;Guzzo, A.; DuBow, M.S.
Mol. Gen. Genet. 242, 455-460, 1994
A;Title: A luxAB transcriptional fusion to the cryptic celF gene of Escherichia coli displays increased luminescence in the presence of nickel.
A;Reference number: S42587; MUID:94166755; PMID:8121401
A;Accession: S42587
A;Molecule type: DNA
A;Residues: 1-11 <GUZ>
C;Genetics:
A;Gene: celF

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AT 2
||
Db 5 AT 6

RESULT 22

S33782

acetolactate synthase (EC 4.1.3.18) small chain, valine-sensitive - *Serratia marcescens* (fragment)

C;Species: *Serratia marcescens*

C;Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999

C;Accession: S33782

R;Yang, J.H.; Kim, S.S.

Biochim. Biophys. Acta 1157, 178-184, 1993

A;Title: Purification and characterization of the valine sensitive acetolactate synthase from *Serratia marcescens* ATCC 25419.

A;Reference number: S33781; MUID:93283409; PMID:8507653

A;Accession: S33782

A;Molecule type: protein

A;Residues: 1-11 <YAN>

A;Experimental source: ATCC 25419

C;Complex: heterotetramer; two small and two large chains

C;Function:

A;Description: catalyzes the condensation of pyruvate and alpha-ketobutyrate to form alpha-aceto-alpha-hydroxybutyrate

A;Pathway: valine, leucine, and isoleucine biosynthesis

A;Note: this isoenzyme exhibits homotropic allosterism with pyruvate

C;Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; flavoprotein; heterotetramer; magnesium; oxo-acid-lyase; valine inhibition

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GR 8
||
Db 5 GR 6

RESULT 23

B41835

translation elongation factor EF-G homolog - *Bacillus subtilis* (fragment)

C;Species: *Bacillus subtilis*

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Dec-1997

C;Accession: B41835

R;Mitchell, C.; Morris, P.W.; Vary, J.C.

J. Bacteriol. 174, 2474-2477, 1992

A;Title: Identification of proteins phosphorylated by ATP during sporulation of *Bacillus subtilis*.

A;Reference number: A41835; MUID:92210489; PMID:1556067

A;Accession: B41835

A;Molecule type: protein

A;Residues: 1-11 <MIT>

A;Note: this protein is phosphorylated during stationary phase but not during exponential growth

C;Keywords: phosphoprotein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KT 6
||
Db 5 KT 6

RESULT 24

S14087

parasporal crystal protein CryIA.b - *Bacillus thuringiensis* (fragments)
N;Alternate names: delta-endotoxin
C;Species: *Bacillus thuringiensis*
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997
C;Accession: S14087
R;Convents, D.; Cherlet, M.; van Damme, J.; Lasters, I.; Lauwereys, M.
Eur. J. Biochem. 195, 631-635, 1991
A;Title: Two structural domains as a general fold of the toxic fragment of the
Bacillus thuringiensis delta-endotoxins.
A;Reference number: S14087; MUID:91153300; PMID:1847865
A;Accession: S14087
A;Molecule type: protein
A;Residues: 1-11 <CON>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TG 7
||
Db 3 TG 4

RESULT 25

A44755

20alpha-hydroxysteroid dehydrogenase (EC 1.1.1.149) - *Clostridium scindens*
(fragment)

C;Species: *Clostridium scindens*
C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 17-Mar-1999
C;Accession: A44755

R;Krafft, A.E.; Hylemon, P.B.
J. Bacteriol. 171, 2925-2932, 1989

A;Title: Purification and characterization of a novel form of 20alpha-
hydroxysteroid dehydrogenase from *Clostridium scindens*.

A;Reference number: A44755; MUID:89255043; PMID:2722736

A;Accession: A44755
A;Molecule type: protein
A;Residues: 1-11 <KRA>

C;Comment: This enzyme was purified to homogeneity and shown to have 20alpha-
hydroxysteroid dehydrogenase activity in the presence of NADH or NADPH. The
enzyme as purified lacked glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
activity although the fragment shows near identity to known GAPDH sequences.

C;Keywords: homotetramer; NAD; NADP; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GR 8
||

Db 10 GR 11

RESULT 26

E41476

probable antigen 5 - *Mycobacterium leprae* (fragment)

C;Species: *Mycobacterium leprae*

C;Date: 10-Apr-1992 #sequence_revision 10-Apr-1992 #text_change 18-Jun-1993

C;Accession: E41476

R;Hartskeerl, R.A.; van Rens, R.M.; Stabel, L.F.E.M.; de Wit, M.Y.L.; Klatser, P.R.

Infect. Immun. 58, 2821-2827, 1990

A;Title: Selection and characterization of recombinant clones that produce *Mycobacterium leprae* antigens recognized by antibodies in sera from household contacts of leprosy patients.

A;Reference number: A41476; MUID:90354041; PMID:1696931

A;Accession: E41476

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-11 <HAR>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11

||

Db 5 PR 6

RESULT 27

S33519

probable secreted protein - *Acholeplasma laidlawii* (fragment)

C;Species: *Acholeplasma laidlawii*

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 22-Oct-1999

C;Accession: S33519

R;Boyer, M.J.; Jarhede, T.K.; Tegman, V.; Wieslander, A.
submitted to the EMBL Data Library, June 1993

A;Description: Sequence regions from *Acholeplasma laidlawii* which restore export of beta-lactamase in *Escherichia coli*.

A;Reference number: S33518

A;Accession: S33519

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <BOY>

A;Cross-references: EMBL:Z22875; NID:g311706; PIDN:CAA80495.1; PID:g311708

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KK 5

||

Db 2 KK 3

RESULT 28

S19775
wound-induced protein - tomato (fragment)
C;Species: Lycopersicon esculentum (tomato)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Sep-1997
C;Accession: S19775
R;Parsons, B.L.
submitted to the EMBL Data Library, May 1991
A;Reference number: S19773
A;Accession: S19775
A;Molecule type: mRNA
A;Residues: 1-11 <PAR>
A;Cross-references: EMBL:X59884; NID:g19323; PID:g19324

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KK 5
||
Db 5 KK 6

RESULT 29
PC4267
ribosomal protein L12.1 - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997
C;Accession: PC4267
R;Kawakami, T.; Kamo, M.; Chen, M.C.; Tsugita, A.
submitted to JIPID, April 1997
A;Reference number: PC4267
A;Accession: PC4267
A;Molecule type: protein
A;Residues: 1-11 <KAW>
A;Experimental source: strain Japonica Nihonbare

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AT 2
||
Db 3 AT 4

RESULT 30
PQ0731
unidentified 5.7/35K protein [imported] - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: PQ0731
R;Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A;Title: A rice protein library; a data-file of rice proteins separated by two-dimensional electrophoresis.
A;Reference number: PQ0696
A;Accession: PQ0731

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <KOM>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AT 2
||
Db 1 AT 2

RESULT 31

PC2173

triacylglycerol lipase (EC 3.1.1.3) II - *Rhizopus niveus* (strain IFO 4759)
(fragments)

C;Species: *Rhizopus niveus*

C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999

C;Accession: PC2173

R;Kohno, M.; Kugimiya, W.; Hashimoto, Y.; Morita, Y.

Biosci. Biotechnol. Biochem. 58, 1007-1012, 1994

A;Title: Purification, characterization, and crystallization of two types of lipase from *Rhizopus niveus*.

A;Reference number: PC2171; MUID:94319059; PMID:7765029

A;Accession: PC2173

A;Molecule type: protein

A;Residues: 1-10;11 <KOH>

C;Comment: This enzyme catalyzes the hydrolysis of the ester bonds of triacylglycerols and the synthesis of ester bonds via transesterification.

C;Comment: This enzyme is produced from lipase I by limited proteolysis due to the action of a serine protease.

C;Keywords: carboxylic ester hydrolase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AT 2
||
Db 9 AT 10

RESULT 32

S78026

ribosomal protein YmL29, mitochondrial - yeast (*Saccharomyces cerevisiae*)
(fragment)

C;Species: *Saccharomyces cerevisiae*

C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 14-Nov-1997

C;Accession: S78026

R;Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wittmann-Liebold, B.; Nishimura, T.; Isono, K.

Eur. J. Biochem. 245, 449-456, 1997

A;Title: Identification and characterization of the genes for mitochondrial ribosomal proteins of *Saccharomyces cerevisiae*.

A;Reference number: S78018; MUID:97296414; PMID:9151978

A;Accession: S78026

A;Molecule type: protein
A;Residues: 1-11 <KIT>
C;Genetics:
A;Genome: nuclear
C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 8 PR 9

RESULT 33

A34135

DNA-binding protein p - Crithidia fasciculata mitochondrion (fragment)
C;Species: mitochondrion Crithidia fasciculata
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 07-Dec-1999
C;Accession: A34135

R;Tittawella, I.

FEBS Lett. 260, 57-61, 1990

A;Title: Kinetoplast DNA-aggregating proteins from the parasitic protozoan
Crithidia fasciculata.

A;Reference number: A34135

A;Accession: A34135

A;Molecule type: protein

A;Residues: 1-11 <tit>

C;Genetics:

A;Genome: mitochondrion

A;Genetic code: SGC6

C;Keywords: mitochondrion

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 7 PR 8

RESULT 34

A61512

variant surface glycoprotein MITat 1.7 - Trypanosoma brucei (fragment)
C;Species: Trypanosoma brucei
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-May-1999
C;Accession: A61512

R;Holder, A.A.; Cross, G.A.M.

Mol. Biochem. Parasitol. 2, 135-150, 1981

A;Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei.
C-terminal location of antigenically cross-reacting carbohydrate moieties.

A;Reference number: A61512; MUID:81172836; PMID:6163983

A;Accession: A61512

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <HOL>
C;Keywords: glycoprotein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TG 7
||
Db 9 TG 10

RESULT 35
A26120
6-phosphofructokinase (EC 2.7.1.11) - pig roundworm (fragment)
N;Alternate names: phosphofructokinase; phosphohexokinase
C;Species: Ascaris suum (pig roundworm)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 28-Apr-1993
C;Accession: A26120
R;Kulkarni, G.; Rao, G.S.J.; Srinivasan, N.G.; Hofer, H.W.; Yuan, P.M.; Harris, B.G.
J. Biol. Chem. 262, 32-34, 1987
A;Title: Ascaris suum phosphofructokinase. Phosphorylation by protein kinase and sequence of the phosphopeptide.
A;Reference number: A26120; MUID:87083467; PMID:3025208
A;Accession: A26120
A;Molecule type: protein
A;Residues: 1-11 <KUL>
C;Keywords: glycolysis; phosphotransferase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GR 8
||
Db 3 GR 4

RESULT 36
A34662
Achatina cardio-excitatory peptide-1 - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 11-Jul-1997
C;Accession: A34662
R;Fujimoto, K.; Ohta, N.; Yoshida, M.; Kubota, I.; Muneoka, Y.; Kobayashi, M.
Biochem. Biophys. Res. Commun. 167, 777-783, 1990
A;Title: A novel cardio-excitatory peptide isolated from the atria of the African giant snail, Achatina fulica.
A;Reference number: A34662; MUID:90211261; PMID:2322251
A;Accession: A34662
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <FUJ>
C;Keywords: amidated carboxyl end
F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GR 8
||
Db 9 GR 10

RESULT 37
S05002
corazonin - American cockroach
C;Species: Periplaneta americana (American cockroach)
C;Date: 07-Sep-1990 #sequence_revision 09-Apr-1998 #text_change 09-Apr-1998
C;Accession: S05002
R;Veenstra, J.A.
FEBS Lett. 250, 231-234, 1989
A;Title: Isolation and structure of corazonin, a cardioactive peptide from the american cockroach.
A;Reference number: S05002; MUID:89325572; PMID:2753132
A;Accession: S05002
A;Molecule type: protein
A;Residues: 1-11 <VEE>
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TN 3
||
Db 10 TN 11

RESULT 38
S33300
probable substance P - smaller spotted catshark
C;Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Mar-1999
C;Accession: S33300
R;Waugh, D.; Wang, Y.; Hazon, N.; Balment, R.J.; Conlon, J.M.
Eur. J. Biochem. 214, 469-474, 1993
A;Title: Primary structures and biological activities of substance-P-related peptides from the brain of the dogfish, Scyliorhinus canicula.
A;Reference number: S33300; MUID:93292508; PMID:7685693
A;Accession: S33300
A;Molecule type: protein
A;Residues: 1-11 <WAU>
A;Experimental source: brain
C;Function:
A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions
A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;1/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 PR 11
||
Db 2 PR 3

RESULT 39

C37196

bradykinin-potentiating peptide 3 - island jararaca

C;Species: Bothrops insularis (island jararaca)

C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994

C;Accession: C37196

R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A;Title: Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.

A;Reference number: A37196; MUID:90351557; PMID:2386615

A;Accession: C37196

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <CIN>

C;Keywords: pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 PR 11
||
Db 5 PR 6

RESULT 40

D37196

bradykinin-potentiating peptide 4 - island jararaca

C;Species: Bothrops insularis (island jararaca)

C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994

C;Accession: D37196

R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A;Title: Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.

A;Reference number: A37196; MUID:90351557; PMID:2386615

A;Accession: D37196

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <CIN>

C;Keywords: pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 5 PR 6

RESULT 41

D57789

gallbladder stone matrix protein, 14.5K - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 23-Feb-1996
C;Accession: D57789
R;Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, February 1996
A;Description: The proteins of gallbladder stones.
A;Reference number: A57789
A;Accession: D57789
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <BIN>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AT 2
||
Db 2 AT 3

RESULT 42

PT0250

Ig heavy chain CRD3 region (clone 2-109B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0250
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain
diversity and joining segments in adult human peripheral blood B lymphocytes.
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0250
A;Molecule type: DNA
A;Residues: 1-11 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GR 8
||
Db 7 GR 8

RESULT 43

PT0273

Ig heavy chain CRD3 region (clone 3-109A) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0273

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and joining segments in adult human peripheral blood B lymphocytes.

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0273

A;Molecule type: DNA

A;Residues: 1-11 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RP 10

||

Db 8 RP 9

RESULT 44

PT0287

Ig heavy chain CRD3 region (clone 4-103) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0287

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and joining segments in adult human peripheral blood B lymphocytes.

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0287

A;Molecule type: DNA

A;Residues: 1-11 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GR 8

||

Db 5 GR 6

RESULT 45

PT0302

Ig heavy chain CRD3 region (clone 5-112) - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0302
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain
diversity and joining segments in adult human peripheral blood B lymphocytes.
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0302
A;Molecule type: DNA
A;Residues: 1-11 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 4 PR 5

RESULT 46
S13279
Ile-Ser-bradykinin - human (fragment)
N;Alternate names: T-kinin
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 24-Jul-1998
C;Accession: S13279
R;Wunderer, G.; Walter, I.; Eschenbacher, B.; Lang, M.; Kellermann, J.;
Kindermann, G.
Biol. Chem. Hoppe-Seyler 371, 977-981, 1990
A;Title: Ile-Ser-bradykinin is an aberrant permeability factor in various human
malignant effusions.
A;Reference number: S13279; MUID:91166748; PMID:2076202
A;Accession: S13279
A;Molecule type: protein
A;Residues: 1-11 <WUN>
C;Keywords: bradykinin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RP 10
||
Db 3 RP 4

RESULT 47
I54193
Rhesus blood group CcEe protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C;Accession: I54193

R;Cherif-Zahar, B.; Le Van Kim, C.; Rouillac, C.; Raynal, V.; Cartron, J.P.; Colin, Y.
Genomics 19, 68-74, 1994
A;Title: Organization of the gene (RHCE) encoding the human blood group RhCcEe antigens and characterization of the promoter region.
A;Reference number: I54193; MUID:94245182; PMID:8188244
A;Accession: I54193
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-11 <RES>
A;Cross-references: GB:S70456; NID:g546795; PIDN:AAD14061.1; PID:g4261761
C;Genetics:
A;Gene: GDB:RHCE
A;Cross-references: GDB:229957; OMIM:111700
A;Map position: 1p36.2-1p34

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RR 9
||
Db 10 RR 11

RESULT 48
S51732
T-cell receptor alpha chain joining region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999
C;Accession: S51732
R;Durinovic-Bello, I.; Steinle, A.; Ziegler, A.G.; Schendel, D.J.
submitted to the EMBL Data Library, November 1993
A;Reference number: S51732
A;Accession: S51732
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-11 <DUR>
A;Cross-references: EMBL:Z28343; NID:g607116; PIDN:CAA82197.1; PID:g607117
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TG 7
||
Db 6 TG 7

RESULT 49
S23926
major glycoprotein PAS-6 - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 01-Feb-1999 #text_change 01-Feb-1999
C;Accession: S23926
R;Kim, D.H.; Kanno, C.; Mizokami, Y.

Biochim. Biophys. Acta 1122, 203-211, 1992
A;Title: Purification and characterization of major glycoproteins, PAS-6 and
PAS-7, from bovine milk fat globule membrane.
A;Reference number: S23926; MUID:92353107; PMID:1643094
A;Accession: S23926
A;Molecule type: protein
A;Residues: 1-11 <KIM>
C;Keywords: glycoprotein; milk; blocked amino end

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NK 4
||
Db 4 NK 5

RESULT 50
S54347
tubulin beta chain - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 27-Oct-1995 #sequence_revision 30-Jan-1998 #text_change 07-May-1999
C;Accession: S54347
R;Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.
Biochem. J. 306, 551-555, 1995
A;Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform
in glial cells.
A;Reference number: S54343; MUID:95194333; PMID:7887910
A;Accession: S54347
A;Molecule type: protein
A;Residues: 1-11 <OKA>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AT 2
||
Db 8 AT 9

RESULT 51
A14454
6-phosphofructokinase (EC 2.7.1.11) - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 28-Apr-1993
C;Accession: A14454
R;Fordyce, A.M.; Midwinter, G.G.; Moore, C.H.
Biochem. Soc. Trans. 7, 721-723, 1979
A;Title: The N-terminal amino acid sequence of sheep heart phosphofructokinase.
A;Reference number: A14454; MUID:80004524; PMID:157899
A;Accession: A14454
A;Molecule type: protein
A;Residues: 1-11 <FOR>
C;Keywords: glycolysis; phosphotransferase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KT 6
||
Db 9 KT 10

RESULT 52

B29806

acidic proline-rich protein HP43a - golden hamster (fragment)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Jun-1993
C;Accession: B29806
R;Mehansho, H.; Ann, D.K.; Butler, L.G.; Rogler, J.; Carlson, D.M.
J. Biol. Chem. 262, 12344-12350, 1987
A;Title: Induction of proline-rich proteins in hamster salivary glands by
isoproterenol treatment and an unusual growth inhibition by tannins.
A;Reference number: A92611; MUID:87308247; PMID:3040740
A;Accession: B29806
A;Molecule type: protein
A;Residues: 1-11 <MEH>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AT 2
||
Db 1 AT 2

RESULT 53

A29806

acidic proline-rich protein HP43b - golden hamster (fragment)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Jun-1993
C;Accession: A29806
R;Mehansho, H.; Ann, D.K.; Butler, L.G.; Rogler, J.; Carlson, D.M.
J. Biol. Chem. 262, 12344-12350, 1987
A;Title: Induction of proline-rich proteins in hamster salivary glands by
isoproterenol treatment and an unusual growth inhibition by tannins.
A;Reference number: A92611; MUID:87308247; PMID:3040740
A;Accession: A29806
A;Molecule type: protein
A;Residues: 1-11 <MEH>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AT 2
||
Db 1 AT 2

RESULT 54
PH1632
Ig H chain V-D-J region (clone B-less 209) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1632
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.
A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1632
A;Molecule type: DNA
A;Residues: 1-11 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 RR 9
||
Db 3 RR 4

RESULT 55
PH1376
T antigen variant K-3 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
C;Accession: PH1376
R;Lill, N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.
J. Exp. Med. 176, 449-457, 1992
A;Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product select for transformed cells with point mutations within sequences encoding CTL recognition epitopes.
A;Reference number: PH1373; MUID:92364547; PMID:1380062
A;Accession: PH1376
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-11 <LIL>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 NK 4
||
Db 5 NK 6

RESULT 56
PT0211
T-cell receptor alpha chain V-J region (4-1-G.4) - mouse (fragment)
C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C;Accession: PT0211
R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted in non-obese diabetic mice.
A;Reference number: PT0209; MUID:91217621; PMID:1902501
A;Accession: PT0211
A;Molecule type: mRNA
A;Residues: 1-11 <NAK>
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TG 7
||
Db 7 TG 8

RESULT 57
C38887
T-cell receptor gamma chain (5a.3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: C38887
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma genes in intestinal intraepithelial lymphocytes from murine athymic chimeras.
A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: C38887
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-11 <WHE>
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GR 8
||
Db 5 GR 6

RESULT 58
S45386
low density lipoprotein receptor-related protein - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Feb-1995 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C;Accession: S45386
R;Herz, J.; Kowal, R.C.; Goldstein, J.L.; Brown, M.S.
EMBO J. 9, 1769-1776, 1990

A;Title: Proteolytic processing of the 600 kd low density lipoprotein receptor-related protein (LRP) occurs in a trans-Golgi compartment.
A;Reference number: S12538; MUID:90269210; PMID:2112085
A;Accession: S45386
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <HER>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TN 3
||
Db 7 TN 8

RESULT 59
S09349
microtubule-associated protein MAP2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 21-Nov-1998
C;Accession: S09349
R;Papandrikopoulou, A.; Doll, T.; Tucker, R.P.; Garner, C.C.; Matus, A.
Nature 340, 650-652, 1989
A;Title: Embryonic MAP2 lacks the cross-linking sidearm sequences and dendritic targeting signal of adult MAP2.
A;Reference number: S09349; MUID:89365159; PMID:2770869
A;Accession: S09349
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-11 <PAP>
C;Genetics:
A;Gene: MAP2

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AT 2
||
Db 5 AT 6

RESULT 60
PH0929
T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0929
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0929
A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: concanavalin A-activated lymphoblast

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RP 10
||
Db 4 RP 5

RESULT 61

PH0938

T-cell receptor beta chain V-D-J region (clone 9) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0938

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0938

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: complete Freund's adjuvant-immunized lymph node

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GR 8
||
Db 7 GR 8

RESULT 62

PH0947

T-cell receptor beta chain V-D-J region (clone A2) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0947

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0947

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein fragment-reactive T-cell, recovered
from experimentally induced allergic encephalomyelitis

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RR 9
||
Db 4 RR 5

RESULT 63
PH0919
T-cell receptor beta chain V-D-J region (isolate 5) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0919
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0919
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
A;Note: the authors translated the codon CAG for residue 11 as Glu
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TG 7
||
Db 9 TG 10

RESULT 64
I52304
gene rSSTR4 protein - rat (fragment)
C;Species: Rattus sp. (rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 17-Mar-1999
C;Accession: I52304
R;Xu, Y.; Bruno, J.F.; Berelowitz, M.
Biochem. Biophys. Res. Commun. 206, 935-941, 1995
A;Title: Characterization of the proximal promoter region of the rat
somatostatin receptor gene, SSTR4.
A;Reference number: I52304; MUID:95134278; PMID:7832807
A;Accession: I52304
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-11 <RES>
A;Cross-references: GB:S75475; NID:g914315
C;Genetics:
A;Gene: rSSTR4

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AT 2
||
Db 5 AT 6

RESULT 65
A48973
glucoamylase A1 (EC 3.2.1.-) - Chalara paradoxa (fragment)
C;Species: Chalara paradoxa
C;Date: 19-Dec-1993 #sequence_revision 25-Apr-1997 #text_change 25-Apr-1997
C;Accession: A48973
R;Monma, M.; Kainuma, K.
Carbohydr. Res. 227, 385-388, 1992
A;Title: Heterogeneity of the glucoamylase components of the raw-starch-digesting amylase from Chalara paradoxa.
A;Reference number: A48973; MUID:92361881; PMID:1499035
A;Accession: A48973
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <MON>
A;Note: sequence extracted from NCBI backbone (NCBIP:110946)
C;Keywords: glycosidase; hydrolase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AT 2
||
Db 1 AT 2

RESULT 66
PN0169
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 03-Jun-2002
C;Accession: PN0169
R;Fukaya, N.; Chow, L.P.; Sugiura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides proteins and the partial amino acid sequence of a peptidyl-prolyl cis-trans isomerase.
A;Reference number: PN0160
A;Accession: PN0169
A;Molecule type: protein
A;Residues: 1-11 <FUK>
A;Experimental source: strain M-1-1
C;Keywords: NAD; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TG 7
 ||
Db 10 TG 11

RESULT 67

S52252

hypothetical protein pco 5'-region - Escherichia coli plasmid pRJ1004 (fragment)
C;Species: Escherichia coli
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: S70166; S52252
R;Brown, N.L.; Barrett, S.R.; Camakaris, J.; Lee, B.T.O.; Rouch, D.A.
Mol. Microbiol. 17, 1153-1166, 1995
A;Title: Molecular genetics and transport analysis of the copper-resistance
determinant (pco) from Escherichia coli plasmid pRJ1004.
A;Reference number: S70159; MUID:96130847; PMID:8594334
A;Accession: S70166
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-11 <BRO>
A;Cross-references: EMBL:X83541; NID:g619126; PIDN:CAA58524.1; PID:g619127
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January
1995
C;Comment: This is the hypothetical translation of a sequence that was not
reported as a coding sequence in the complete genome.
C;Genetics:
A;Genome: plasmid pRJ1004

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AT 2
 ||
Db 7 AT 8

RESULT 68

S19015

hypothetical protein 11 ruvC-yebC intergenic region - Escherichia coli
C;Species: Escherichia coli
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: S19015
R;Sharples, G.J.; Lloyd, R.G.
J. Bacteriol. 173, 7711-7715, 1991
A;Title: Resolution of Holliday junctions in Escherichia coli: identification of
the ruvC gene product as a 19-kilodalton protein.
A;Reference number: S19013; MUID:92041688; PMID:1657895
A;Accession: S19015
A;Molecule type: DNA
A;Residues: 1-11 <SHA>
A;Cross-references: EMBL:X59551; NID:g42172; PIDN:CAA42127.1; PID:g42174
C;Comment: This is the hypothetical translation of a sequence that was not
reported as a coding sequence in the complete genome.

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 RP 10
||
Db 2 RP 3

RESULT 69

ECLQ2M

tachykinin II - migratory locust
C;Species: *Locusta migratoria* (migratory locust)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Dec-1995
C;Accession: S08266
R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; de Loof, A.
FEBS Lett. 261, 397-401, 1990
A;Title: Locustatachykinin I and II, two novel insect neuropeptides with
homology to peptides of the vertebrate tachykinin family.
A;Reference number: S08265; MUID:90184489; PMID:2311766
A;Accession: S08266
A;Molecule type: protein
A;Residues: 1-11 <SCH>
C;Superfamily: tachykinin
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;11/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 A 1
|
Db 1 A 1

RESULT 70

EOOCC

eledoisin - curled octopus
C;Species: *Eledone cirrosa*, *Ozaena cirrosa* (curled octopus)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Mar-1998
C;Accession: B01561; A01561
R;Anastasi, A.; Erspamer, V.
Arch. Biochem. Biophys. 101, 56-65, 1963
A;Title: The isolation and amino acid sequence of eledoisin, the active
endecapeptide of the posterior salivary glands of Eledone.
A;Reference number: A01561
A;Accession: B01561
A;Molecule type: protein
A;Residues: 1-11 <ANA>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland;
secretagogue; vasodilator; venom
F;11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 P 10
|
Db 2 P 2

RESULT 71

EOOC

eledoisin - musky octopus

C;Species: Eledone moschata, Ozaena moschata (musky octopus)

C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 20-Mar-1998

C;Accession: A01561

R;Anastasi, A.; Erspamer, V.

Arch. Biochem. Biophys. 101, 56-65, 1963

A;Title: The isolation and amino acid sequence of eledoisin, the active endecapeptide of the posterior salivary glands of Eledone.

A;Reference number: A01561

A;Accession: A01561

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland; secretagogue; vasodilator; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 P 10
|
Db 2 P 2

RESULT 72

GMROL

leucosulfakinin - Madeira cockroach

N;Alternate names: LSK

C;Species: Leucophaea maderae (Madeira cockroach)

C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 13-Sep-1996

C;Accession: A01622

R;Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.

Science 234, 71-73, 1986

A;Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and cholecystokinin.

A;Reference number: A01622; MUID:86315858; PMID:3749893

A;Accession: A01622

A;Molecule type: protein

A;Residues: 1-11 <NAC>

C;Superfamily: gastrin

C;Keywords: amidated carboxyl end; hormone; sulfoprotein

F;6/Binding site: sulfate (Tyr) (covalent) #status experimental

F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 G 7
|
Db 7 G 7

RESULT 73
LFTWWE
probable trpEG leader peptide - *Thermus aquaticus*
C;Species: *Thermus aquaticus*
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
C;Accession: S03315
R;Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.
Biochim. Biophys. Acta 950, 303-312, 1988
A;Title: Molecular cloning and nucleotide sequence of *Thermus thermophilus* HB8
trpE and trpG.
A;Reference number: S03315; MUID:89000781; PMID:2844259
A;Accession: S03315
A;Molecule type: DNA
A;Residues: 1-11 <SAT>
A;Cross-references: EMBL:X07744; NID:g48261; PIDN:CAA30565.1; PID:g48262
A;Note: the source is designated as *Thermus thermophilus* HB8
C;Genetics:
A;Gene: trpL
C;Superfamily: probable trpEG leader peptide

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 A 1
|
Db 2 A 2

RESULT 74
S66196
alcohol dehydrogenase (EC 1.1.1.1) class III high affinity form - cod (*Gadus*
sp.) (fragment)
C;Species: *Gadus* sp. (cod)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 12-Jun-1998
C;Accession: S66196
R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.;
Hendrickson, R.C.; Michel, H.; Shabanowitz, J.; Hunt, D.F.; Joernvall, H.
FEBS Lett. 367, 237-240, 1995
A;Title: Multiplicity of N-terminal structures of medium-chain alcohol
dehydrogenases. Mass-spectrometric analysis of plant, lower vertebrate and
higher vertebrate class I, II, and III forms of the enzyme.
A;Reference number: S66191; MUID:95331382; PMID:7607314
A;Accession: S66196
A;Molecule type: protein
A;Residues: 1-11 <HJE>
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 9.1%; Score 1; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 T 2
|
Db 1 T 1

RESULT 75

G42762

proteasome endopeptidase complex (EC 3.4.25.1) subunit 13 - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Feb-2003

C;Accession: G42762

R;Dick, L.R.; Moomaw, C.R.; Pramanik, B.C.; DeMartino, G.N.; Slaughter, C.A.

Biochemistry 31, 7347-7355, 1992

A;Title: Identification and localization of a cysteinyl residue critical for the trypsin-like catalytic activity of the proteasome.

A;Reference number: A42762; MUID:92378961; PMID:1510924

A;Accession: G42762

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <DIC>

A;Note: sequence extracted from NCBI backbone (NCBIP:112176)

C;Superfamily: multicatalytic endopeptidase complex chain C9

C;Keywords: hydrolase

Query Match 9.1%; Score 1; DB 2; Length 11;

Best Local Similarity 100.08%; Pred. No. 2.1e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 T 2
|
Db 3 T 3

Search completed: April 8, 2004, 15:49:25

Job time : 8.61538 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:47:33 ; Search time 30.3077 Seconds
(without alignments)
95.432 Million cell updates/sec

Title: US-09-787-443A-9

Perfect score: 11

Sequence: 1 ATNKKTGRRPR 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1073127 seqs, 262937947 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9223

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : Published_Applications_AA:*

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

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14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4	36.4	11	10	US-09-775-052-55	Sequence 55, Appl
3	4	36.4	11	10	US-09-775-052-57	Sequence 57, Appl
4	4	36.4	11	14	US-10-108-795-29	Sequence 29, Appl
5	4	36.4	11	14	US-10-115-365-29	Sequence 29, Appl
6	4	36.4	11	14	US-10-116-212-29	Sequence 29, Appl
7	4	36.4	11	15	US-10-391-155-4	Sequence 4, Appli
8	3	27.3	11	9	US-09-850-373-1	Sequence 1, Appli
9	3	27.3	11	9	US-09-853-530A-5	Sequence 5, Appli
10	3	27.3	11	9	US-09-871-961-2	Sequence 2, Appli
11	3	27.3	11	9	US-09-845-667-1	Sequence 1, Appli
12	3	27.3	11	9	US-09-820-893-116	Sequence 116, App
13	3	27.3	11	9	US-09-873-676-16	Sequence 16, Appl
14	3	27.3	11	9	US-09-976-165-54	Sequence 54, Appl
15	3	27.3	11	9	US-09-736-743A-2	Sequence 2, Appli
16	3	27.3	11	9	US-09-753-126-131	Sequence 131, App
17	3	27.3	11	9	US-09-753-126-133	Sequence 133, App
18	3	27.3	11	9	US-09-953-587-31	Sequence 31, Appl
19	3	27.3	11	9	US-09-250-611-21	Sequence 21, Appl
20	3	27.3	11	9	US-09-839-743-16	Sequence 16, Appl
21	3	27.3	11	9	US-09-839-743-17	Sequence 17, Appl
22	3	27.3	11	9	US-09-839-743-18	Sequence 18, Appl
23	3	27.3	11	9	US-09-839-743-20	Sequence 20, Appl
24	3	27.3	11	9	US-09-839-743-21	Sequence 21, Appl
25	3	27.3	11	9	US-09-839-743-22	Sequence 22, Appl
26	3	27.3	11	9	US-09-839-743-23	Sequence 23, Appl
27	3	27.3	11	9	US-09-969-192-19	Sequence 19, Appl
28	3	27.3	11	9	US-09-985-936-6	Sequence 6, Appli
29	3	27.3	11	9	US-09-955-504-29	Sequence 29, Appl
30	3	27.3	11	9	US-09-851-138-109	Sequence 109, App
31	3	27.3	11	9	US-09-851-138-110	Sequence 110, App
32	3	27.3	11	9	US-09-851-138-112	Sequence 112, App
33	3	27.3	11	9	US-09-851-138-114	Sequence 114, App
34	3	27.3	11	9	US-09-851-138-115	Sequence 115, App
35	3	27.3	11	9	US-09-851-138-118	Sequence 118, App
36	3	27.3	11	9	US-09-851-138-119	Sequence 119, App
37	3	27.3	11	10	US-09-880-505-7	Sequence 7, Appli
38	3	27.3	11	10	US-09-999-724-76	Sequence 76, Appl
39	3	27.3	11	10	US-09-948-193-20	Sequence 20, Appl
40	3	27.3	11	10	US-09-791-393-264	Sequence 264, App
41	3	27.3	11	10	US-09-988-792-8	Sequence 8, Appli
42	3	27.3	11	10	US-09-791-389-264	Sequence 264, App
43	3	27.3	11	10	US-09-896-896A-95	Sequence 95, Appl
44	3	27.3	11	10	US-09-896-896A-97	Sequence 97, Appl
45	3	27.3	11	10	US-09-226-402-31	Sequence 31, Appl
46	3	27.3	11	10	US-09-876-904A-38	Sequence 38, Appl
47	3	27.3	11	10	US-09-876-904A-62	Sequence 62, Appl
48	3	27.3	11	10	US-09-876-904A-111	Sequence 111, App
49	3	27.3	11	10	US-09-876-904A-113	Sequence 113, App
50	3	27.3	11	10	US-09-876-904A-239	Sequence 239, App
51	3	27.3	11	10	US-09-876-904A-246	Sequence 246, App
52	3	27.3	11	10	US-09-876-904A-354	Sequence 354, App
53	3	27.3	11	10	US-09-876-904A-389	Sequence 389, App
54	3	27.3	11	10	US-09-876-904A-436	Sequence 436, App
55	3	27.3	11	10	US-09-852-910-160	Sequence 160, App
56	3	27.3	11	10	US-09-852-910-189	Sequence 189, App

57	3	27.3	11	10	US-09-852-910-192	Sequence 192, App
58	3	27.3	11	10	US-09-954-385-283	Sequence 283, App
59	3	27.3	11	10	US-09-791-524-62	Sequence 62, Appl
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61	3	27.3	11	10	US-09-940-316B-35	Sequence 35, Appl
62	3	27.3	11	10	US-09-940-316B-39	Sequence 39, Appl
63	3	27.3	11	10	US-09-940-316B-41	Sequence 41, Appl
64	3	27.3	11	10	US-09-940-316B-53	Sequence 53, Appl
65	3	27.3	11	11	US-09-933-780C-10	Sequence 10, Appl
66	3	27.3	11	12	US-10-406-031-29	Sequence 29, Appl
67	3	27.3	11	12	US-10-398-104-159	Sequence 159, App
68	3	27.3	11	12	US-10-398-104-267	Sequence 267, App
69	3	27.3	11	12	US-10-607-565-116	Sequence 116, App
70	3	27.3	11	12	US-10-149-135-168	Sequence 168, App
71	3	27.3	11	12	US-10-149-135-203	Sequence 203, App
72	3	27.3	11	12	US-10-149-135-232	Sequence 232, App
73	3	27.3	11	12	US-10-149-135-258	Sequence 258, App
74	3	27.3	11	12	US-10-149-135-584	Sequence 584, App
75	3	27.3	11	12	US-10-149-135-614	Sequence 614, App
76	3	27.3	11	12	US-10-149-135-799	Sequence 799, App
77	3	27.3	11	12	US-10-149-135-957	Sequence 957, App
78	3	27.3	11	12	US-10-149-135-1144	Sequence 1144, Ap
79	3	27.3	11	12	US-10-149-135-1155	Sequence 1155, Ap
80	3	27.3	11	12	US-10-149-135-1172	Sequence 1172, Ap
81	3	27.3	11	13	US-10-125-452-29	Sequence 29, Appl
82	3	27.3	11	13	US-10-051-643-7	Sequence 7, Appli
83	3	27.3	11	14	US-10-108-795-26	Sequence 26, Appl
84	3	27.3	11	14	US-10-108-795-28	Sequence 28, Appl
85	3	27.3	11	14	US-10-180-326-5	Sequence 5, Appli
86	3	27.3	11	14	US-10-115-365-26	Sequence 26, Appl
87	3	27.3	11	14	US-10-115-365-28	Sequence 28, Appl
88	3	27.3	11	14	US-10-059-261-31	Sequence 31, Appl
89	3	27.3	11	14	US-10-059-261-139	Sequence 139, App
90	3	27.3	11	14	US-10-006-869-1387	Sequence 1387, Ap
91	3	27.3	11	14	US-10-006-869-1417	Sequence 1417, Ap
92	3	27.3	11	14	US-10-006-869-1462	Sequence 1462, Ap
93	3	27.3	11	14	US-10-006-869-1492	Sequence 1492, Ap
94	3	27.3	11	14	US-10-006-869-1537	Sequence 1537, Ap
95	3	27.3	11	14	US-10-006-869-1811	Sequence 1811, Ap
96	3	27.3	11	14	US-10-006-869-1826	Sequence 1826, Ap
97	3	27.3	11	14	US-10-006-869-1841	Sequence 1841, Ap
98	3	27.3	11	14	US-10-006-869-1856	Sequence 1856, Ap
99	3	27.3	11	14	US-10-006-869-1871	Sequence 1871, Ap
100	3	27.3	11	14	US-10-006-869-1957	Sequence 1957, Ap

ALIGNMENTS

RESULT 1

US-09-802-109-7

; Sequence 7, Application US/09802109

; Patent No. US20020058611A1

; GENERAL INFORMATION:

; APPLICANT: Stein, Stanley

; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC

; FILE REFERENCE: 601-1-083

; CURRENT APPLICATION NUMBER: US/09/802,109
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 09/044,411
; PRIOR FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: Same as Sequence ID 2, but with a substitution of
; OTHER INFORMATION: Gln to Pro.
; NAME/KEY: BINDING
; LOCATION: (10)
; OTHER INFORMATION: Cys(biotin)
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.
; OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-802-109-7

Query Match 36.4%; Score 4; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
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Db 4 RRPR 7

RESULT 2
US-09-775-052-55
; Sequence 55, Application US/09775052
; Publication No. US20030054000A1
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48881/1742
; CURRENT APPLICATION NUMBER: US/09/775,052
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 09/208,966
; PRIOR FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: 60/082,402
; PRIOR FILING DATE: 1998-04-20
; PRIOR APPLICATION NUMBER: 60/069,012
; PRIOR FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human
US-09-775-052-55

Query Match 36.4%; Score 4; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
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Db 6 RRPR 9

RESULT 3

US-09-775-052-57

; Sequence 57, Application US/09775052
; Publication No. US20030054000A1
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48881/1742
; CURRENT APPLICATION NUMBER: US/09/775,052
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 09/208,966
; PRIOR FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: 60/082,402
; PRIOR FILING DATE: 1998-04-20
; PRIOR APPLICATION NUMBER: 60/069,012
; PRIOR FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human

US-09-775-052-57

Query Match 36.4%; Score 4; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
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Db 6 RRPR 9

RESULT 4

US-10-108-795-29

; Sequence 29, Application US/10108795
; Publication No. US20030033633A1
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A
; APPLICANT: Millward, Thomas A
; TITLE OF INVENTION: Calcium Regulated Kinase
; FILE REFERENCE: 30110
; CURRENT APPLICATION NUMBER: US/10/108,795
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 09/133,062
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: GB 9717089.8
; PRIOR FILING DATE: 1997-08-12
; PRIOR APPLICATION NUMBER: GB 9717499.9
; PRIOR FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic peptide
; OTHER INFORMATION: internal peptide
US-10-108-795-29

Query Match 36.4%; Score 4; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKTG 7
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Db 4 KKTG 7

RESULT 5
US-10-115-365-29
; Sequence 29, Application US/10115365
; Publication No. US20030074694A1
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A
; APPLICANT: Millward, Thomas A
; TITLE OF INVENTION: Calcium Regulated Kinase
; FILE REFERENCE: 30110
; CURRENT APPLICATION NUMBER: US/10/115,365
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 09/133,062
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: GB 9717499.9
; PRIOR FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic peptide
; OTHER INFORMATION: internal peptide
US-10-115-365-29

Query Match 36.4%; Score 4; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKTG 7
|||
Db 4 KKTG 7

RESULT 6
US-10-116-212-29
; Sequence 29, Application US/10116212
; Publication No. US20030163844A1

; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A
; APPLICANT: Millward, Thomas A
; TITLE OF INVENTION: Calcium Regulated Kinase
; FILE REFERENCE: 30110
; CURRENT APPLICATION NUMBER: US/10/116,212
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US/09/133,062
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: GB 9717089.8
; PRIOR FILING DATE: 1997-08-12
; PRIOR APPLICATION NUMBER: GB 9717499.9
; PRIOR FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic peptide
; OTHER INFORMATION: internal peptide
US-10-116-212-29

Query Match 36.4%; Score 4; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKTG 7
 ||||
Db 4 KKTG 7

RESULT 7
US-10-391-155-4
; Sequence 4, Application US/10391155
; Publication No. US20040009463A1
; GENERAL INFORMATION:
; APPLICANT: Simons, Michael
; Gao, Youhe
; TITLE OF INVENTION: Method for PR-39 peptide mediated
; selective inhibition of IKBA degradation
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Prashker, Esq.
; STREET: P.O. Box 5387
; CITY: Magnolia
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01930
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
; COMPUTER: Dell PC
; OPERATING SYSTEM: MS XP
; SOFTWARE: WordPerfect version 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/391,155

;
; FILING DATE: 18-Mar-2003
; CLASSIFICATION: Unknown
;
; ATTORNEY/AGENT INFORMATION:
; NAME: David Prashker, Esq.
; REGISTRATION NUMBER: 29,693
; REFERENCE/DOCKET NUMBER: BIS-044/D
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (978) 525-3794
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-391-155-4

Query Match 36.4%; Score 4; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRPR 11
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Db 2 RRPR 5

RESULT 8
US-09-850-373-1
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; Sequence 1, Application US/09850373
; Patent No. US20010051605A1
;
; GENERAL INFORMATION:
; APPLICANT: Strayer, David S
; TITLE OF INVENTION: Epidermal Growth Factor Inhibitor
; FILE REFERENCE: JEFF-0226-DIV
; CURRENT APPLICATION NUMBER: US/09/850,373
; CURRENT FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: 08/530,340
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: PCT/US94/03675
; PRIOR FILING DATE: 1994-04-04
; PRIOR APPLICATION NUMBER: 08/041,774
; PRIOR FILING DATE: 1993-04-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
;
; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: Description of Artificial Sequence: An epidermal
; OTHER INFORMATION: growth factor inhibitor peptide
US-09-850-373-1

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKT 6
|||
Db 8 KKT 10

RESULT 9
US-09-853-530A-5
; Sequence 5, Application US/09853530A
; Patent No. US20020048590A1
; GENERAL INFORMATION:
; APPLICANT: Klimpel, Kurt
; Goletz, Theresa J.
; Arora, Naveen
; Leppla, Stephen H.
; Berzofsky, Jay A.
; TITLE OF INVENTION: Targeting Antigens to the MHC Class I
; Processing Pathway With an Anthrax Toxin Fusion
Protein
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/853,530A
; FILING DATE: 09-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 015280-290100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-853-530A-5

Query Match 27.3%; Score 3; DB 9; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
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Db 4 GRR 6

RESULT 10

US-09-871-961-2

; Sequence 2, Application US/09871961
; Patent No. US20020061544A1
; GENERAL INFORMATION:
; APPLICANT: SARMA, Puranam U.
; APPLICANT: MADAN, Taruna
; APPLICANT: PRIYADARSINY, Priyanka
; APPLICANT: KATTI, Seturam B.
; APPLICANT: HAQ, Wahajul
; TITLE OF INVENTION: NOVEL POLYPEPTIDES USEFUL FOR DIAGNOSIS OF ASPERGILLUS
; TITLE OF INVENTION: FUMIGATUS AND A PROCESS OF PREPARING THE SAME
; FILE REFERENCE: 2761-115P
; CURRENT APPLICATION NUMBER: US/09/871,961
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus

US-09-871-961-2

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TNK 4
|||
Db 5 TNK 7

RESULT 11

US-09-845-667-1

; Sequence 1, Application US/09845667
; Patent No. US20020065221A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Philip
; Alessi, Dario
; Cross, Darren
; TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD
; FOR AGENTS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Braman & Rogalskyj, LLP
; STREET: P.O. Box 352
; CITY: Canandaigua
; STATE: New York
; COUNTRY: USA

ZIP: 14424-0352
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/845,667
FILING DATE: 30-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/091,763
FILING DATE: 19-JUN-1998
APPLICATION NUMBER: PCT/GB96/03186
FILING DATE: 20-DEC-1996
APPLICATION NUMBER: GB 9526083.2
FILING DATE: 20-DEC-1995
APPLICATION NUMBER: GB 9610272.8
FILING DATE: 16-MAY-1996
APPLICATION NUMBER: GB 9615066.9
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 002.00041
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-393-3002
TELEFAX: 716-393-3001
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-845-667-1

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 2 RPR 4

RESULT 12
US-09-820-893-116
Sequence 116, Application US/09820893
Patent No. US20020076705A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 31 Human Secreted Proteins
FILE REFERENCE: PZ033P1
CURRENT APPLICATION NUMBER: US/09/820,893
CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: 09/531,119
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/102,895
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 116
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-820-893-116

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 3 RPR 5

RESULT 13
US-09-873-676-16
; Sequence 16, Application US/09873676
; Patent No. US20020077289A1
; GENERAL INFORMATION:
; APPLICANT: MacDonald, Nicholas J.
; APPLICANT: Sim, Kim L.
; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use
; FILE REFERENCE: 05213-0378 (43170-259333)
; CURRENT APPLICATION NUMBER: US/09/873,676
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,065
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/289,387
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic binding peptide
US-09-873-676-16

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 3 RPR 5

RESULT 14

US-09-976-165-54
; Sequence 54, Application US/09976165
; Patent No. US20020107383A1
; GENERAL INFORMATION:
; APPLICANT: FUJIWARA, TSUTOMU
; APPLICANT: WATANABE, TAKESHI
; APPLICANT: HORIE, MASATO
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
; TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
; FILE REFERENCE: Q-53599
; CURRENT APPLICATION NUMBER: US/09/976,165
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/565,538
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 09/055,699
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/820,170
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: JP 63410/1996
; PRIOR FILING DATE: 1996-03-19
; PRIOR APPLICATION NUMBER: JP 69163/1997
; PRIOR FILING DATE: 1997-03-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Bovine sp.

US-09-976-165-54

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATN 3
|||
Db 1 ATN 3

RESULT 15

US-09-736-743A-2
; Sequence 2, Application US/09736743A
; Patent No. US20020110869A1
; GENERAL INFORMATION:
; APPLICANT: KOVESDI, IMRE
; APPLICANT: BRUDER, JOSEPH T
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING CHIMERIC PROTEIN AND RELATED
VECTOR, CELL AND
; TITLE OF INVENTION: METHOD OF EXPRESSION
; FILE REFERENCE: 203591
; CURRENT APPLICATION NUMBER: US/09/736,743A
; CURRENT FILING DATE: 2000-12-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT

; ORGANISM: Human immunodeficiency virus
US-09-736-743A-2

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 8 RRP 10

RESULT 16

US-09-753-126-131

; Sequence 131, Application US/09753126
; Patent No. US20020127219A1
; GENERAL INFORMATION:
; APPLICANT: OKKELS, JENS SIGURD
; APPLICANT: JENSEN, ANNE DAM
; APPLICANT: HALKIER, TORBEN
; APPLICANT: JENSEN, RIKKE BOLDING
; TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES AND LYSOSOMAL ENZYME
; TITLE OF INVENTION: ACTIVATORS
; FILE REFERENCE: 31-000600US
; CURRENT APPLICATION NUMBER: US/09/753,126
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PA 1999 01891
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 60/174,652
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: PA 200 00865
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/210,984
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: 60/211,124
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: PA 2000 01027
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/217,497
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 131
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide

US-09-753-126-131

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TNK 4
|||

Db 8 TNK 10

RESULT 17

US-09-753-126-133

; Sequence 133, Application US/09753126

; Patent No. US20020127219A1

; GENERAL INFORMATION:

; APPLICANT: OKKELS, JENS SIGURD

; APPLICANT: JENSEN, ANNE DAM

; APPLICANT: HALKIER, TORBEN

; APPLICANT: JENSEN, RIKKE BOLDING

; TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES AND LYSOSOMAL ENZYME

; TITLE OF INVENTION: ACTIVATORS

; FILE REFERENCE: 31-000600US

; CURRENT APPLICATION NUMBER: US/09/753,126

; CURRENT FILING DATE: 2001-06-11

; PRIOR APPLICATION NUMBER: PA 1999 01891

; PRIOR FILING DATE: 1999-12-30

; PRIOR APPLICATION NUMBER: 60/174,652

; PRIOR FILING DATE: 2000-01-06

; PRIOR APPLICATION NUMBER: PA 200 00865

; PRIOR FILING DATE: 2000-06-02

; PRIOR APPLICATION NUMBER: 60/210,984

; PRIOR FILING DATE: 2000-06-12

; PRIOR APPLICATION NUMBER: 60/211,124

; PRIOR FILING DATE: 2000-06-12

; PRIOR APPLICATION NUMBER: PA 2000 01027

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: 60/217,497

; PRIOR FILING DATE: 2000-07-11

; NUMBER OF SEQ ID NOS: 147

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 133

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: peptide

US-09-753-126-133

Query Match 27.3%; Score 3; DB 9; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATN 3

|||

Db 7 ATN 9

RESULT 18

US-09-953-587-31

; Sequence 31, Application US/09953587

; Patent No. US20020142939A1

; GENERAL INFORMATION:

; APPLICANT: CHADA, Kiran K.

; APPLICANT: ASHAR, Hena
; APPLICANT: TKACHENKO, Alex
; APPLICANT: ZHOU, Xianjin
; TITLE OF INVENTION: HMGI PROTEINS IN CANCER AND OBESITY
; FILE REFERENCE: 267/110
; CURRENT APPLICATION NUMBER: US/09/953,587
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 08/852,666
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: US 08/679,529
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: PCT/US/97/21299
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-953-587-31

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 4 RPR 6

RESULT 19
US-09-250-611-21
; Sequence 21, Application US/09250611
; Patent No. US20020143161A1
; GENERAL INFORMATION:
; APPLICANT: Byrne, Jennifer A.
; APPLICANT: Basset, Paul
; TITLE OF INVENTION: Members of the D52 Gene Family
; FILE REFERENCE: 1383.0210001
; CURRENT APPLICATION NUMBER: US/09/250,611
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)..(2)
; OTHER INFORMATION: May be any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (8)
; OTHER INFORMATION: May be any amino acid
US-09-250-611-21

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKT 6
|||
Db 5 KKT 7

RESULT 20

US-09-839-743-16

; Sequence 16, Application US/09839743
; Patent No. US20020146824A1
; GENERAL INFORMATION:
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Lamb, Christopher
; APPLICANT: Doerner, Peter
; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. US20020146824A1el Transcription Enhancer Element and
; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
; FILE REFERENCE: SALKINS.008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/189,344
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Nicotiana tabacum

US-09-839-743-16

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 4 RPR 6

RESULT 21

US-09-839-743-17

; Sequence 17, Application US/09839743
; Patent No. US20020146824A1
; GENERAL INFORMATION:
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Lamb, Christopher
; APPLICANT: Doerner, Peter
; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. US20020146824A1el Transcription Enhancer Element and
; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof

; FILE REFERENCE: SALKINS.008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/189,344
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-839-743-17

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 8 RPR 10

RESULT 22
US-09-839-743-18
; Sequence 18, Application US/09839743
; Patent No. US20020146824A1
; GENERAL INFORMATION:
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Lamb, Christopher
; APPLICANT: Doerner, Peter
; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. US20020146824A1el Transcription Enhancer Element and
; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
; FILE REFERENCE: SALKINS.008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/189,344
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-839-743-18

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 4 RPR 6

RESULT 23

US-09-839-743-20

; Sequence 20, Application US/09839743
; Patent No. US20020146824A1
; GENERAL INFORMATION:
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Lamb, Christopher
; APPLICANT: Doerner, Peter
; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. US20020146824A1el Transcription Enhancer Element and
; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
; FILE REFERENCE: SALKINS.008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/189,344
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Nicotiana tabacum

US-09-839-743-20

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 4 RRP 6

RESULT 24

US-09-839-743-21

; Sequence 21, Application US/09839743
; Patent No. US20020146824A1
; GENERAL INFORMATION:
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Lamb, Christopher
; APPLICANT: Doerner, Peter
; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. US20020146824A1el Transcription Enhancer Element and
; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
; FILE REFERENCE: SALKINS.008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19

; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/189,344
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-839-743-21

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 4 RRP 6

RESULT 25

US-09-839-743-22

; Sequence 22, Application US/09839743
; Patent No. US20020146824A1
; GENERAL INFORMATION:
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Lamb, Christopher
; APPLICANT: Doerner, Peter
; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. US20020146824A1 Transcription Enhancer Element and
; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
; FILE REFERENCE: SALKINS.008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/189,344
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-839-743-22

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
|||

Db

4 GRR 6

RESULT 26

US-09-839-743-23

; Sequence 23, Application US/09839743

; Patent No. US20020146824A1

; GENERAL INFORMATION:

; APPLICANT: The Salk Institute for Biological Sciences

; APPLICANT: Lamb, Christopher

; APPLICANT: Doerner, Peter

; APPLICANT: Laible, Goetz

; TITLE OF INVENTION: No. US20020146824A1 Transcription Enhancer Element and

; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof

; FILE REFERENCE: SALKINS.008DV3

; CURRENT APPLICATION NUMBER: US/09/839,743

; CURRENT FILING DATE: 2001-04-19

; PRIOR APPLICATION NUMBER: US 09/401,336

; PRIOR FILING DATE: 1999-09-21

; PRIOR APPLICATION NUMBER: US 09/189,344

; PRIOR FILING DATE: 1998-11-10

; PRIOR APPLICATION NUMBER: US 08/669,721

; PRIOR FILING DATE: 1996-06-27

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 23

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Nicotiana tabacum

US-09-839-743-23

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9

|||

Db 4 GRR 6

RESULT 27

US-09-969-192-19

; Sequence 19, Application US/09969192

; Patent No. US20020151027A1

; GENERAL INFORMATION:

; APPLICANT: WICKHAM, THOMAS J.

; ROELVINK, PETRUS W.

; KOVESDI, IMRE

; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF

; CONSTRAINED PEPTIDE MOTIFS

; NUMBER OF SEQUENCES: 80

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Leydig, Voit & Mayer, Ltd.

; STREET: Two Prudential Plaza - 49th Floor

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

;

ZIP: 60601

;

COMPUTER READABLE FORM:

;

MEDIUM TYPE: Floppy disk

;

COMPUTER: IBM PC compatible

;

OPERATING SYSTEM: PC-DOS/MS-DOS

;

SOFTWARE: PatentIn Release #1.0, Version #1.30

;

CURRENT APPLICATION DATA:

;

APPLICATION NUMBER: US/09/969,192

;

FILING DATE: 01-Oct-2001

;

PRIOR APPLICATION DATA:

;

APPLICATION NUMBER: US 9-455061

;

FILING DATE: 06-DEC-1999

;

APPLICATION NUMBER: US 9-130225

;

FILING DATE: 06-AUG-1998

;

APPLICATION NUMBER: US 8-701124

;

FILING DATE: 21-AUG-1996

;

ATTORNEY/AGENT INFORMATION:

;

NAME: Hefner, M. Daniel

;

REGISTRATION NUMBER: 41,826

;

REFERENCE/DOCKET NUMBER: 213564

;

INFORMATION FOR SEQ ID NO: 19:

;

SEQUENCE CHARACTERISTICS:

;

LENGTH: 11 amino acids

;

TYPE: amino acid

;

TOPOLOGY: linear

;

MOLECULE TYPE: peptide

;

SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-09-969-192-19

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKT 6
|||
Db 8 KKT 10

RESULT 28

US-09-985-936-6

;

Sequence 6, Application US/09985936

;

Patent No. US20020164696A1

;

GENERAL INFORMATION:

;

APPLICANT: Stefan KAPPELER

;

APPLICANT: Zakaria FARAH

;

APPLICANT: Johannes Maarten van den BRINK

;

APPLICANT: Henrik RAHBEK-NIELSEN

;

APPLICANT: Peter BUDTZ

;

TITLE OF INVENTION: Method of producing non-bovine chymosin

;

TITLE OF INVENTION: and use hereof

;

FILE REFERENCE: KAPPELER=1A

;

CURRENT APPLICATION NUMBER: US/09/985,936

;

CURRENT FILING DATE: 2001-11-06

;

PRIOR APPLICATION NUMBER: US 09/705,917

;

PRIOR FILING DATE: 2000-11-06

;

NUMBER OF SEQ ID NOS: 7

;

SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chymosin hydrolyzes the peptide bond between
; OTHER INFORMATION: nitrophenylalanine and Ile.
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (8)..(8)
; OTHER INFORMATION: Xaa = nitrophenylalanine
US-09-985-936-6

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 1 RPR 3

RESULT 29
US-09-955-504-29
; Sequence 29, Application US/09955504
; Publication No. US20020182702A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: ADAM Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT006P2
; CURRENT APPLICATION NUMBER: US/09/955,504
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,222
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 09/712,907
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: PCT/US00/14308
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/178,717
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/142,930
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/136,388
; PRIOR FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-504-29

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11

Db 2 RPR 4

|||
RESULT 30
US-09-851-138-109
; Sequence 109, Application US/09851138
; Publication No. US20020183508A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND
DIAGNOSTIC
; AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,138
; FILING DATE: 09-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,075
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 109:
US-09-851-138-109

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10

|||

Db 2 RRP 4

RESULT 31
US-09-851-138-110
; Sequence 110, Application US/09851138
; Publication No. US20020183508A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND
DIAGNOSTIC
; AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,138
; FILING DATE: 09-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,075
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-09-851-138-110

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 2 RRP 4

RESULT 32
US-09-851-138-112
; Sequence 112, Application US/09851138
; Publication No. US20020183508A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND
DIAGNOSTIC
; AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,138
; FILING DATE: 09-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,075
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-09-851-138-112

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGR 8
|||
Db 5 TGR 7

RESULT 33
US-09-851-138-114
; Sequence 114, Application US/09851138
; Publication No. US20020183508A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND
DIAGNOSTIC
; AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,138
; FILING DATE: 09-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,075
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-09-851-138-114

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 TGR 8
|||
Db 5 TGR 7

RESULT 34
US-09-851-138-115
; Sequence 115, Application US/09851138
; Publication No. US20020183508A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND
DIAGNOSTIC
; AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,138
; FILING DATE: 09-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,075
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-09-851-138-115

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGR 8
 |||
Db 5 TGR 7

RESULT 35

US-09-851-138-118
; Sequence 118, Application US/09851138
; Publication No. US20020183508A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND
DIAGNOSTIC
; AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,138
; FILING DATE: 09-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,075
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 118:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 118:
US-09-851-138-118

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGR 8
|||
Db 5 TGR 7

RESULT 36
US-09-851-138-119

; Sequence 119, Application US/09851138
; Publication No. US20020183508A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND
DIAGNOSTIC
; AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,138
; FILING DATE: 09-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,075
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 119:
US-09-851-138-119

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGR 8
|||
Db 5 TGR 7

RESULT 37
US-09-880-505-7
; Sequence 7, Application US/09880505

; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880,505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-880-505-7

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGR 8
|||
Db 9 TGR 11

RESULT 38

US-09-999-724-76
; Sequence 76, Application US/09999724
; Publication No. US20030022355A1
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; APPLICANT: KOVESDI, IMRE
; APPLICANT: BROUGH, DOUGLAS E.
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER
; FILE REFERENCE: 212960
; CURRENT APPLICATION NUMBER: US/09/999,724
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/101,751
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: WO 96US19150
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 08/700,846
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/701,124
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/563,368
; PRIOR FILING DATE: 1995-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 11

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-999-724-76

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKT 6
|||
Db 8 KKT 10

RESULT 39

US-09-948-193-20

; Sequence 20, Application US/09948193
; Publication No. US20030027335A1
; GENERAL INFORMATION:
; APPLICANT: Ruley, H. Earl
; APPLICANT: Jo, Daewoong
; TITLE OF INVENTION: Genome Engineering by Cell-Permeable DNA
; TITLE OF INVENTION: Site-Specific Recombinases
; FILE REFERENCE: 22000.0109U2
; CURRENT APPLICATION NUMBER: US/09/948,193
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/230,690
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Description: MTS from HIV Tat
US-09-948-193-20

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGR 8
|||
Db 1 TGR 3

RESULT 40

US-09-791-393-264

; Sequence 264, Application US/09791393
; Publication No. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for

; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder
(BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 264
; LENGTH: 11
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-264

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGR 8
|||
Db 9 TGR 11

RESULT 41

US-09-988-792-8

; Sequence 8, Application US/09988792
; Publication No. US20030032599A1
; GENERAL INFORMATION:
; APPLICANT: Lipkowski, Andrezej W
; APPLICANT: Carr, Daniel B
; TITLE OF INVENTION: NOVEL ANTIMICROBIAL COMPOUNDS
; FILE REFERENCE: 18475-025
; CURRENT APPLICATION NUMBER: US/09/988,792
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,369
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-988-792-8

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 1 RPR 3

RESULT 42

US-09-791-389-264

; Sequence 264, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder
(BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 264
; LENGTH: 11
; TYPE: PRT
; ORGANISM: homo sapien

US-09-791-389-264

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGR 8
|||
Db 9 TGR 11

RESULT 43

US-09-896-896A-95

; Sequence 95, Application US/09896896A
; Publication No. US20030036181A1
; GENERAL INFORMATION:
; APPLICANT: MAXYGEN APS
; TITLE OF INVENTION: PEPTIDE EXTENDED GLYCOSYLATED POLYPEPTIDES
; FILE REFERENCE: 0217us210
; CURRENT APPLICATION NUMBER: US/09/896,896A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/217,497
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/225,558
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: DK PA 2000 01027

; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DK PA 2000 01092
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: PCT/DK00/00743
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: PCT/DK01/00090
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-896-896A-95

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TNK 4
|||
Db 8 TNK 10

RESULT 44
US-09-896-896A-97
; Sequence 97, Application US/09896896A
; Publication No. US20030036181A1
; GENERAL INFORMATION:
; APPLICANT: MAXYGEN APS
; TITLE OF INVENTION: PEPTIDE EXTENDED GLYCOSYLATED POLYPEPTIDES
; FILE REFERENCE: 0217us210
; CURRENT APPLICATION NUMBER: US/09/896,896A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/217,497
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/225,558
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: DK PA 2000 01027
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DK PA 2000 01092
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: PCT/DK00/00743
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: PCT/DK01/00090
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: peptide
US-09-896-896A-97

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATN 3
|||
Db 7 ATN 9

RESULT 45

US-09-226-402-31

; Sequence 31, Application US/09226402
; Publication No. US20030051260A1
; GENERAL INFORMATION:
; APPLICANT: Chada, Kiran K.
; APPLICANT: Ashar, Hena
; APPLICANT: Tkachenko, Alex
; APPLICANT: Zhou, Xianjin
; TITLE OF INVENTION: HMG1 Proteins in Cancer and Obesity
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Muccino
; STREET: 758 Springfield Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/226,402
; FILING DATE: 06 JAN 1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Muccino, Richard R.
; REGISTRATION NUMBER: 32,538
; REFERENCE/DOCKET NUMBER: UMD1 037CIPCIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 273 4988
; TELEFAX: (908) 273 4679
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO

US-09-226-402-31

Query Match 27.3%; Score 3; DB 10; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 4 RPR 6

RESULT 46
US-09-876-904A-38
; Sequence 38, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Adenovirus
; OTHER INFORMATION: type 2/5 Ela peptide
US-09-876-904A-38

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 8 RPR 10

RESULT 47
US-09-876-904A-62
; Sequence 62, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A

; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Adenovirus
type
; OTHER INFORMATION: 2/5 Ela peptide
US-09-876-904A-62

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 8 RPR 10

RESULT 48

US-09-876-904A-111
; Sequence 111, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HIV Tat
protein
US-09-876-904A-111

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||

Db 9 RRP 11

RESULT 49

US-09-876-904A-113

; Sequence 113, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic c-Myc and
HIV
; OTHER INFORMATION: Tat NLSs

US-09-876-904A-113

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10

|||

Db 9 RRP 11

RESULT 50

US-09-876-904A-239

; Sequence 239, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 239
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Hydrophilic protein
US-09-876-904A-239

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKT 6
|||
Db 4 KKT 6

RESULT 51
US-09-876-904A-246
; Sequence 246, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 246
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: mismatch repair peptide
US-09-876-904A-246

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
|||
Db 2 GRR 4

RESULT 52
US-09-876-904A-354
; Sequence 354, Application US/09876904A
; Publication No. US20030072794A1

; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 354
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human ATF-3 (in basic region that binds DNA)
US-09-876-904A-354

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NKK 5
|||
Db 5 NKK 7

RESULT 53
US-09-876-904A-389
; Sequence 389, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 389
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; OTHER INFORMATION: C. elegans Sdc-3 protein.
US-09-876-904A-389

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKT 6
|||
Db 9 KKT 11

RESULT 54
US-09-876-904A-436
; Sequence 436, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 436
; LENGTH: 11
; TYPE: PRT
; ORGANISM: *Caenorhabditis elegans*
; FEATURE:
; OTHER INFORMATION: *C. elegans* sex-determining *Tra-1* protein.
US-09-876-904A-436

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
|||
Db 4 GRR 6

RESULT 55
US-09-852-910-160
; Sequence 160, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
; APPLICANT: Hamm, Heidi
; APPLICANT: Gilchrist, Annette
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled
Receptor Signaling
; FILE REFERENCE: 2661-101
; CURRENT APPLICATION NUMBER: US/09/852,910
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472

; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 160
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(11)
; OTHER INFORMATION: G alpha t library peptide
US-09-852-910-160

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NKK 5
|||
Db 4 NKK 6

RESULT 56

US-09-852-910-189

; Sequence 189, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
; APPLICANT: Hamm, Heidi
; APPLICANT: Gilchrist, Annette
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor Signaling
; FILE REFERENCE: 2661-101
; CURRENT APPLICATION NUMBER: US/09/852,910
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 189
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(11)
; OTHER INFORMATION: Gs library peptide
US-09-852-910-189

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 2 RPR 4

RESULT 57
US-09-852-910-192
; Sequence 192, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
; APPLICANT: Hamm, Heidi
; APPLICANT: Gilchrist, Annette
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor Signaling
; FILE REFERENCE: 2661-101
; CURRENT APPLICATION NUMBER: US/09/852,910
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 192
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(11)
; OTHER INFORMATION: Gs library peptide
US-09-852-910-192

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 5 RRP 7

RESULT 58
US-09-954-385-283
; Sequence 283, Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gastel, Franciscus J.C.
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Huaming
; APPLICANT: Winetzky, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; TITLE OF INVENTION: Complexes
; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/09/954,385
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 283
; LENGTH: 11
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-283

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KTG 7
|||
Db 4 KTG 6

RESULT 59
US-09-791-524-62
; Sequence 62, Application US/09791524
; Publication No. US20030143209A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Products Inc.
; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of
Heterologous Genes
; FILE REFERENCE: A3319A
; CURRENT APPLICATION NUMBER: US/09/791,524
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/09828
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 62
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Adenovirus
US-09-791-524-62

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TNK 4
|||
Db 7 TNK 9

RESULT 60
US-09-791-524-109
; Sequence 109, Application US/09791524
; Publication No. US20030143209A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Products Inc.
; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of
Heterologous Genes
; FILE REFERENCE: A3319A
; CURRENT APPLICATION NUMBER: US/09/791,524
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/09828
; PRIOR FILING DATE: 1998-08-27

; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 109
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Adenovirus
US-09-791-524-109

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TNK 4
|||
Db 7 TNK 9

RESULT 61
US-09-940-316B-35
; Sequence 35, Application US/09940316B
; Publication No. US20030175901A1
; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTI, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDES ENCODING THE *fkba* GENE OF THE FK-520
POLYKETIDE SYNTHASE
; TITLE OF INVENTION: GENE CLUSTER
; FILE REFERENCE: 30062-20026.11
; CURRENT APPLICATION NUMBER: US/09/940,316B
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/410,551
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
; OTHER INFORMATION: synthase fragment
US-09-940-316B-35

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 2 RPR 4

RESULT 62

US-09-940-316B-39

; Sequence 39, Application US/09940316B
; Publication No. US20030175901A1
; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTI, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDES ENCODING THE fkba GENE OF THE FK-520
POLYKETIDE SYNTHASE
; TITLE OF INVENTION: GENE CLUSTER
; FILE REFERENCE: 30062-20026.11
; CURRENT APPLICATION NUMBER: US/09/940,316B
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/410,551
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
; OTHER INFORMATION: synthase fragment

US-09-940-316B-39

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 5 RRP 7

RESULT 63

US-09-940-316B-41

; Sequence 41, Application US/09940316B
; Publication No. US20030175901A1
; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER

; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTI, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDES ENCODING THE fkba GENE OF THE FK-520
POLYKETIDE SYNTHASE
; TITLE OF INVENTION: GENE CLUSTER
; FILE REFERENCE: 30062-20026.11
; CURRENT APPLICATION NUMBER: US/09/940,316B
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/410,551
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
; OTHER INFORMATION: synthase fragment
US-09-940-316B-41

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 2 RPR 4

RESULT 64
US-09-940-316B-53
; Sequence 53, Application US/09940316B
; Publication No. US20030175901A1
; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTI, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDES ENCODING THE fkba GENE OF THE FK-520
POLYKETIDE SYNTHASE
; TITLE OF INVENTION: GENE CLUSTER
; FILE REFERENCE: 30062-20026.11
; CURRENT APPLICATION NUMBER: US/09/940,316B
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/410,551
; PRIOR FILING DATE: 1999-10-01

; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
; OTHER INFORMATION: synthase fragment
US-09-940-316B-53

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 2 RPR 4

RESULT 65
US-09-933-780C-10
; Sequence 10, Application US/09933780C
; Publication No. US20030229202A1
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PHARMACEUTICALS INC.
; APPLICANT: GUO, Yong
; APPLICANT: MORSE, Clarence C
; APPLICANT: YAO, Zhengbin
; TITLE OF INVENTION: MEMBRANE PENETRATING PEPTIDES AND USES THEREOF
; FILE REFERENCE: HMR2053 PCT
; CURRENT APPLICATION NUMBER: US/09/933,780C
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/227,647
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: GB 0103110.3
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of intracellular loop of 5HT2A receptor
US-09-933-780C-10

Query Match 27.3%; Score 3; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATN 3
|||
Db 9 ATN 11

RESULT 66

US-10-406-031-29

; Sequence 29, Application US/10406031
; Publication No. US20040043017A1
; GENERAL INFORMATION:
; APPLICANT: Masci, Paul Pantaleone
; APPLICANT: De Jersey, John
; APPLICANT: Lavin, Martin
; TITLE OF INVENTION: PROTHROMBIN ACTIVATING PROTEIN
; FILE REFERENCE: 15685-002001
; CURRENT APPLICATION NUMBER: US/10/406,031
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: AU 2003901033
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: AU PS1483
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 1
; OTHER INFORMATION: Xaa = any amino acid residue
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide

US-10-406-031-29

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGR 8
|||
Db 8 TGR 10

RESULT 67

US-10-398-104-159

; Sequence 159, Application US/10398104
; Publication No. US20040047880A1
; GENERAL INFORMATION:
; APPLICANT: De Bolle, Xavier Thomas
; APPLICANT: Letesson, Jean-Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Mertens, Pascal Yvon
; APPLICANT: Poolman, Jan
; APPLICANT: Voet, Pierre
; TITLE OF INVENTION: COMPONENT FOR VACCINE
; FILE REFERENCE: B45242

; CURRENT APPLICATION NUMBER: US/10/398,104
; CURRENT FILING DATE: 2003-01-04
; PRIOR APPLICATION NUMBER: PCT/EP01/11409
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: GB 0024200.8
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LOS peptide mimotope sequence
US-10-398-104-159

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GRR 9
|||
Db 8 GRR 10

RESULT 68
US-10-398-104-267
; Sequence 267, Application US/10398104
; Publication No. US20040047880A1
; GENERAL INFORMATION:
; APPLICANT: De Bolle, Xavier Thomas
; APPLICANT: Letesson, Jean-Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Mertens, Pascal Yvon
; APPLICANT: Poolman, Jan
; APPLICANT: Voet, Pierre
; TITLE OF INVENTION: COMPONENT FOR VACCINE
; FILE REFERENCE: B45242
; CURRENT APPLICATION NUMBER: US/10/398,104
; CURRENT FILING DATE: 2003-01-04
; PRIOR APPLICATION NUMBER: PCT/EP01/11409
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: GB 0024200.8
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 267
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LOS peptide mimotope sequence
US-10-398-104-267

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10
|||
Db 3 RRP 5

RESULT 69
US-10-607-565-116
; Sequence 116, Application US/10607565
; Publication No. US20040048294A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 31 Human Secreted Proteins
; FILE REFERENCE: PZ033P1
; CURRENT APPLICATION NUMBER: US/10/607,565
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/531,119
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/101,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/102,895
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 116
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-607-565-116

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 3 RPR 5

RESULT 70
US-10-149-135-168
; Sequence 168, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545

; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-168

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KTG 7
|||
Db 1 KTG 3

RESULT 71
US-10-149-135-203
; Sequence 203, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04

; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 203
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-203

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KTG 7
|||
Db 6 KTG 8

RESULT 72
US-10-149-135-232
; Sequence 232, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 232
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-232

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KTG 7
|||
Db 5 KTG 7

RESULT 73
US-10-149-135-258
; Sequence 258, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 258
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide

US-10-149-135-258

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KTG 7
|||
Db 4 KTG 6

RESULT 74

US-10-149-135-584

; Sequence 584, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 584
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide

US-10-149-135-584

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KTG 7

|||
Db 1 KTG 3

RESULT 75
US-10-149-135-614
; Sequence 614, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 614
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-614

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KTG 7
|||
Db 5 KTG 7

Search completed: April 8, 2004, 16:35:44
Job time : 40.3077 secs

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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 27.7692 Seconds
(without alignments)
124.984 Million cell updates/sec

Title: US-09-787-443A-9

Perfect score: 11

Sequence: 1 ATNKKTGRRPR 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 460

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SPTREMBL_25:
1: sp_archea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rat:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				
No.	Score	Match	Length	DB	ID

Description

1	4	36.4	11	11	Q62207	Q62207 mus musculu
2	3	27.3	11	2	Q9L4F7	Q914f7 bacillus ce
3	3	27.3	11	4	Q15997	Q15997 homo sapien
4	3	27.3	11	4	Q8TDA8	Q8tda8 homo sapien
5	3	27.3	11	5	Q8MPQ3	Q8mpq3 caenorhabdi
6	3	27.3	11	6	Q9GL48	Q9gl48 sus scrofa
7	3	27.3	11	8	Q8MAZ1	Q8maz1 maripa pani
8	3	27.3	11	8	Q8MB39	Q8mb39 wilsonia hu
9	3	27.3	11	8	Q8MB58	Q8mb58 seddera hir
10	3	27.3	11	8	Q8MAZ3	Q8maz3 maripa repe
11	3	27.3	11	8	Q8MBE1	Q8mbel ipomoea alb
12	3	27.3	11	8	Q8MB77	Q8mb77 odonellia h
13	3	27.3	11	8	Q8MB79	Q8mb79 aniseia arg
14	3	27.3	11	8	Q8MB97	Q8mb97 merremia pe
15	3	27.3	11	15	Q9DZ32	Q9dz32 human immun
16	2	18.2	11	2	Q9AIY6	Q9aiy6 carsonella
17	2	18.2	11	2	Q9R790	Q9r790 borrelia ga
18	2	18.2	11	2	Q47451	Q47451 escherichia
19	2	18.2	11	2	Q9R7U8	Q9r7u8 pseudomonas
20	2	18.2	11	2	Q9S618	Q9s618 prochloroco
21	2	18.2	11	2	Q9EUZ3	Q9euz3 escherichia
22	2	18.2	11	2	Q8RMI8	Q8rmi8 enterococcu
23	2	18.2	11	2	Q8KTN1	Q8ktn1 candidatus
24	2	18.2	11	2	P71228	P71228 escherichia
25	2	18.2	11	2	Q9K332	Q9k332 staphylococ
26	2	18.2	11	2	Q9RFZ2	Q9rfz2 mycoplasma
27	2	18.2	11	2	Q47604	Q47604 escherichia
28	2	18.2	11	2	Q47345	Q47345 escherichia
29	2	18.2	11	2	Q47420	Q47420 escherichia
30	2	18.2	11	2	Q44090	Q44090 acholeplasm
31	2	18.2	11	2	Q56413	Q56413 escherichia
32	2	18.2	11	2	Q47059	Q47059 escherichia
33	2	18.2	11	2	Q8GMU3	Q8gmu3 acinetobact
34	2	18.2	11	2	P83537	P83537 lactobacill
35	2	18.2	11	4	Q9NY38	Q9ny38 homo sapien
36	2	18.2	11	4	O60761	O60761 homo sapien
37	2	18.2	11	4	Q9H4H5	Q9h4h5 homo sapien
38	2	18.2	11	4	Q9UCR1	Q9ucr1 homo sapien
39	2	18.2	11	5	Q9UAR8	Q9uar8 aedes aegyp
40	2	18.2	11	5	Q9NL65	Q9nl65 ascaris suu
41	2	18.2	11	5	P82698	P82698 leucophaea
42	2	18.2	11	5	P82699	P82699 leucophaea
43	2	18.2	11	5	P82700	P82700 leucophaea
44	2	18.2	11	5	Q86D32	Q86d32 trypanosoma
45	2	18.2	11	5	Q86D31	Q86d31 trypanosoma
46	2	18.2	11	5	Q95PX6	Q95px6 caenorhabdi
47	2	18.2	11	6	Q9TRW5	Q9trw5 bos taurus
48	2	18.2	11	6	Q9TRX0	Q9trx0 sus scrofa
49	2	18.2	11	7	O77876	O77876 oreochromis
50	2	18.2	11	7	Q29831	Q29831 homo sapien
51	2	18.2	11	7	O19718	O19718 homo sapien
52	2	18.2	11	8	Q94VG8	Q94vg8 varanus gou
53	2	18.2	11	8	Q9G5Y6	Q9g5y6 agama agama
54	2	18.2	11	8	Q9G679	Q9g679 hypsilurus
55	2	18.2	11	8	Q94VI5	Q94vi5 varanus exa
56	2	18.2	11	8	Q94V74	Q94v74 lanthanotus
57	2	18.2	11	8	Q9GH12	Q9gh12 pandorina m

58	2	18.2	11	8	Q94VE7	Q94ve7 varanus kom
59	2	18.2	11	8	Q94VB8	Q94vb8 varanus sal
60	2	18.2	11	8	Q94VH7	Q94vh7 varanus gil
61	2	18.2	11	8	Q94VK1	Q94vk1 varanus aca
62	2	18.2	11	8	Q7YKD8	Q7ykd8 ribes oxyac
63	2	18.2	11	8	Q7YKC6	Q7ykc6 ribes cereu
64	2	18.2	11	8	Q7YKA6	Q7yka6 itea ilicif
65	2	18.2	11	8	Q7Y9D1	Q7y9d1 tympanocryp
66	2	18.2	11	8	Q7Y9B6	Q7y9b6 amphiboluru
67	2	18.2	11	9	Q38415	Q38415 bacteriopha
68	2	18.2	11	9	Q37925	Q37925 bacteriopha
69	2	18.2	11	10	Q06626	Q06626 solanum tub
70	2	18.2	11	10	Q9T0L9	Q9t019 brassica ol
71	2	18.2	11	10	Q8RUE7	Q8rue7 zea mays (m
72	2	18.2	11	10	Q04131	Q04131 lycopersico
73	2	18.2	11	10	P83092	P83092 spinacia ol
74	2	18.2	11	10	Q7X9Y3	Q7x9y3 cucumis sat
75	2	18.2	11	11	Q99JC3	Q99jc3 rattus sp.
76	2	18.2	11	11	Q9QXM6	Q9qxm6 mus musculu
77	2	18.2	11	11	P97755	P97755 rattus norv
78	2	18.2	11	11	Q99N81	Q99n81 mus musculu
79	2	18.2	11	11	Q9R1N6	Q9r1n6 mus musculu
80	2	18.2	11	11	Q60807	Q60807 mus musculu
81	2	18.2	11	11	Q9QYF6	Q9qyf6 mus musculu
82	2	18.2	11	11	Q9Z1H5	Q9z1h5 mus musculu
83	2	18.2	11	11	Q8R2J7	Q8r2j7 mesocricetu
84	2	18.2	11	11	Q80WI3	Q80wi3 rattus sp.
85	2	18.2	11	12	Q86866	Q86866 lymphocytic
86	2	18.2	11	12	Q8JS92	Q8js92 hepatitis b
87	2	18.2	11	12	P89269	P89269 xestia c-ni
88	2	18.2	11	12	Q86864	Q86864 lymphocytic
89	2	18.2	11	12	Q997C1	Q997c1 east africa
90	2	18.2	11	12	Q66877	Q66877 feline cali
91	2	18.2	11	12	Q86868	Q86868 lymphocytic
92	2	18.2	11	12	O40974	O40974 cauliflower
93	2	18.2	11	13	Q9PS22	Q9ps22 xenopus lae
94	2	18.2	11	13	Q90WA2	Q90wa2 gallus gall
95	2	18.2	11	13	Q800X7	Q800x7 chelydra se
96	2	18.2	11	15	Q83410	Q83410 mouse mamma
97	1	9.1	11	2	O68237	O68237 borrelia bu
98	1	9.1	11	2	Q48933	Q48933 mycobacteri
99	1	9.1	11	2	Q9AIZ7	Q9aiz7 carsonella
100	1	9.1	11	2	Q8RKN1	Q8rkn1 escherichia

ALIGNMENTS

RESULT 1

Q62207

ID Q62207

PRELIMINARY;

PRT; 11 AA.

AC Q62207;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Schwannomin (Fragment).

GN NF2.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95072570; PubMed=7981675;
 RA Huynh D.P., Nechiporuk T., Pulst S.-M.;
 RT "Alternative transcripts in the mouse neurofibromatosis type 2 (NF2)
 RT gene are conserved and code for schwannomin with distinct C-terminal
 RT domains.";
 RL Hum. Mol. Genet. 3:1075-1079(1994).
 DR EMBL; L28838; AAA57151.1; -.
 DR PIR; I54368; I54368.
 DR MGD; MGI:97307; Nf2.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1238 MW; C51FA05774140866 CRC64;

 Query Match 36.4%; Score 4; DB 11; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 7 GRRP 10
 ||||
 Db 5 GRRP 8

RESULT 2
 Q9L4F7
 ID Q9L4F7 PRELIMINARY; PRT; 11 AA.
 AC Q9L4F7;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Phosphatidylinositol-specific phospholipase C (PI-PLC)
 DE (Fragment).
 GN PLCA.
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 14579 type strain;
 RX MEDLINE=20055637; PubMed=10589720;
 RA Okstad O., Gominet M., Purnelle B., Rose M., Lereclus D., Kolsto A.B.;
 RT "Sequence analysis of three *Bacillus cereus* loci under PICR-regulated
 RT genes encoding degradative enzymes and enterotoxin.";
 RL Microbiology 145:3129-3138(1999).
 DR EMBL; AJ243711; CAB69804.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1335 MW; 4277A30E20572333 CRC64;

 Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NKK 5
|||
Db 3 NKK 5

RESULT 3

Q15997

ID Q15997 PRELIMINARY; PRT; 11 AA.
AC Q15997;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RARA protein (Fragment).
GN RARA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93222087; PubMed=7682097;
RA Dong S., Geng J.P., Tong J.H., Wu Y., Cai J.R., Sun G.L., Chen S.R.,
RA Wang Z.Y., Larsen C.J., Berger R., et al;
RT "Breakpoint clusters of the PML gene in acute promyelocytic leukemia:
RT primary structure of the reciprocal products of the PML-RARA gene in a
RT patient with t(15;17).";
RL Genes Chromosomes Cancer 6:133-139(1993).
DR EMBL; S57794; AAD13888.1; -.
DR PIR; I54081; I54081.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1277 MW; 33C70E22CDDDC417 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RPR 11
|||
Db 3 RPR 5

RESULT 4

Q8TDA8

ID Q8TDA8 PRELIMINARY; PRT; 11 AA.
AC Q8TDA8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Glutathione synthetase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Cho Y.-W., Lee Y.-Y., Lim C.-J.;
RT "Cloning and characterization of glutathione synthetase gene from

RT human placenta DNA.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF485789; AAL91591.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1235 MW; 1CE28D1E35B86374 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATN 3
|||
Db 2 ATN 4

RESULT 5
Q8MPQ3
ID Q8MPQ3 PRELIMINARY; PRT; 11 AA.
AC Q8MPQ3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein Y23H5A.8b.
GN Y23H5A.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Waterston R.;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Dempsey S., Le T.T.;
RT "The sequence of C. elegans cosmid Y23H5A.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF077541; AAM54173.1; -.
DR WormPep; Y23H5A.8b; CE31097.
KW Hypothetical protein.
SQ SEQUENCE 11 AA; 1319 MW; 6920D63A21B77414 CRC64;

Query Match 27.3%; Score 3; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRP 10

|||
Db 4 RRP 6

RESULT 6

Q9GL48

ID Q9GL48 PRELIMINARY; PRT; 11 AA.
AC Q9GL48;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE G protein-coupled receptor (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Nagasaka T., Boulday G., Coupel S., Coulon F., Tesson L.,
RA Heslan J.-M., Soullou J.-P., Charreau B.;
RT "Alternative double screening for differentially expressed genes by
RT modified RNA differential display and semi-quantitative Reverse
RT Northern blot.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF319662; AAG33870.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1298 MW; 822261F10861BB41 CRC64;

Query Match 27.3%; Score 3; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGR 8
|||
Db 6 TGR 8

RESULT 7

Q8MAZ1

ID Q8MAZ1 PRELIMINARY; PRT; 11 AA.
AC Q8MAZ1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PsbJ (Fragment).
GN PSBJ.
OS Maripa paniculata.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;
OC lamiids; Solanales; Convolvulaceae; Maripa.
OX NCBI_TaxID=197411;
RN [1]
RP SEQUENCE FROM N.A.
RA Stefanovic S., Krueger L., Olmstead R.G.;

RT "Monophyly of the Convolvulaceae and circumscription of their major
RT lineages based on DNA sequences of multiple chloroplast loci.";
RL Am. J. Bot. 0:0-0(2002).
DR EMBL; AY100937; AAM55869.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;
Query Match 27.3%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGR 8
|||
Db 5 TGR 7

RESULT 8
Q8MB39
ID Q8MB39 PRELIMINARY; PRT; 11 AA.
AC Q8MB39;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PsbJ (Fragment).
GN PSBJ.
OS Wilsonia humilis.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;
OC lamiids; Solanales; Convolvulaceae; Wilsonia.
OX NCBI_TaxID=197481;
RN [1]
RP SEQUENCE FROM N.A.
RA Stefanovic S., Krueger L., Olmstead R.G.;
RT "Monophyly of the Convolvulaceae and circumscription of their major
RT lineages based on DNA sequences of multiple chloroplast loci.";
RL Am. J. Bot. 0:0-0(2002).
DR EMBL; AY100914; AAM55777.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 TGR 8
|||
Db 5 TGR 7

RESULT 9
Q8MB58
ID Q8MB58 PRELIMINARY; PRT; 11 AA.

AC Q8MB58;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PsbJ (Fragment).
GN PSBJ.
OS Seddera hirsuta.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;
OC lamiids; Solanales; Convolvulaceae; Seddera.
OX NCBI_TaxID=197444;
RN [1]
RP SEQUENCE FROM N.A.
RA Stefanovic S., Krueger L., Olmstead R.G.;
RT "Monophyly of the Convolvulaceae and circumscription of their major
lineages based on DNA sequences of multiple chloroplast loci.";
RL Am. J. Bot. 0:0-0(2002).
DR EMBL; AY100905; AAM55743.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 27.38; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGR 8
|||
Db 5 TGR 7

RESULT 10
Q8MAZ3
ID Q8MAZ3 PRELIMINARY; PRT; 11 AA.
AC Q8MAZ3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PsbJ (Fragment).
GN PSBJ.
OS Maripa repens.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;
OC lamiids; Solanales; Convolvulaceae; Maripa.
OX NCBI_TaxID=197412;
RN [1]
RP SEQUENCE FROM N.A.
RA Stefanovic S., Krueger L., Olmstead R.G.;
RT "Monophyly of the Convolvulaceae and circumscription of their major
lineages based on DNA sequences of multiple chloroplast loci.";
RL Am. J. Bot. 0:0-0(2002).
DR EMBL; AY100936; AAM55865.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.

FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGR 8
|||
Db 5 TGR 7

RESULT 11

Q8MBE1

ID Q8MBE1 PRELIMINARY; PRT; 11 AA.
AC Q8MBE1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PsbJ (Fragment).
GN PSBJ.
OS Ipomoea alba.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;
OC lamiids; Solanales; Convolvulaceae; Ipomoea.
OX NCBI_TaxID=89634;

RN [1]

RP SEQUENCE FROM N.A.

RA Stefanovic S., Krueger L., Olmstead R.G.;

RT "Monophyly of the Convolvulaceae and circumscription of their major
lineages based on DNA sequences of multiple chloroplast loci.";

RL Am. J. Bot. 0:0-0 (2002).

DR EMBL; AY100861; AAM55568.1; -.

DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.

FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGR 8
|||
Db 5 TGR 7

RESULT 12

Q8MB77

ID Q8MB77 PRELIMINARY; PRT; 11 AA.
AC Q8MB77;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PsbJ (Fragment).
GN PSBJ.

OS Odonellia hirtiflora.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;
OC lamiids; Solanales; Convolvulaceae; Odonellia.
OX NCBI_TaxID=197424;
RN [1]
RP SEQUENCE FROM N.A.
RA Stefanovic S., Krueger L., Olmstead R.G.;
RT "Monophyly of the Convolvulaceae and circumscription of their major
RT lineages based on DNA sequences of multiple chloroplast loci.";
RL Am. J. Bot. 0:0-0 (2002).
DR EMBL; AY100897; AAM55711.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGR 8
|||
Db 5 TGR 7

RESULT 13
Q8MB79
ID Q8MB79 PRELIMINARY; PRT; 11 AA.
AC Q8MB79;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PsbJ (Fragment).
GN PSBJ.
OS Aniseia argentina.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;
OC lamiids; Solanales; Convolvulaceae; Aniseia.
OX NCBI_TaxID=197349;
RN [1]
RP SEQUENCE FROM N.A.
RA Stefanovic S., Krueger L., Olmstead R.G.;
RT "Monophyly of the Convolvulaceae and circumscription of their major
RT lineages based on DNA sequences of multiple chloroplast loci.";
RL Am. J. Bot. 0:0-0 (2002).
DR EMBL; AY100895; AAM55703.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGR 8
|||
Db 5 TGR 7

RESULT 14

Q8MB97

ID Q8MB97 PRELIMINARY; PRT; 11 AA.
AC Q8MB97;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PsbJ (Fragment).
GN PSBJ.
OS Merremia peltata.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;
OC lamiids; Solanales; Convolvulaceae; Merremia.
OX NCBI_TaxID=197416;
RN [1]
RP SEQUENCE FROM N.A.
RA Stefanovic S., Krueger L., Olmstead R.G.;
RT "Monophyly of the Convolvulaceae and circumscription of their major
RT lineages based on DNA sequences of multiple chloroplast loci.";
RL Am. J. Bot. 0:0-0(2002).
DR EMBL; AY100885; AAM55663.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGR 8
|||
Db 5 TGR 7

RESULT 15

Q9DZ32

ID Q9DZ32 PRELIMINARY; PRT; 11 AA.
AC Q9DZ32;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gag polyprotein (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461476; PubMed=11005867;

RA Martinez-Picado J., DePasquale M.P., Kartsonis N., Hanna G.J.,
RA Wong J., Finzi D., Rosenberg E., Gunthard H.F., Sutton L., Savara A.,
RA Petropoulos C.J., Hellmann N., Walker B.D., Richman D.D.,
RA Siliciano R., D'Aquila R.T.;
RT "Antiretroviral resistance during successful therapy of HIV type 1
infection.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:10948-10953(2000).
DR EMBL; AF292799; AAG25407.1; -.
KW Polyprotein.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1386 MW; 79DC73C0145771B4 CRC64;

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGR 8
|||
Db 2 TGR 4

RESULT 16

Q9AIY6

ID Q9AIY6 PRELIMINARY; PRT; 11 AA.
AC Q9AIY6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tryptophanyl-tRNA synthetase (Fragment).
GN TRPS.
OS Carsonella ruddii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.
OX NCBI_TaxID=114186;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20336438; PubMed=10877784;
RA Thao M.L., Moran N.A., Abbot P., Brennan E.B., Burckhardt D.H.,
RA Baumann P.;
RT "Cospeciation of psyllids and their primary prokaryotic
RT endosymbionts.";
RL Appl. Environ. Microbiol. 66:2898-2905(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21125546; PubMed=11222582;
RA Clark M.A., Baumann L., Thao M.L., Moran N.A., Baumann P.;
RT "Degenerative Minimalism in the Genome of a Psyllid Endosymbiont.";
RL J. Bacteriol. 183:1853-1861(2001).
DR EMBL; AF211138; AAK15388.1; -.
DR GO; GO:0004812; F:tRNA ligase activity; IEA.
KW Aminoacyl-tRNA synthetase.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1295 MW; 0CA993A5345B5720 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NK 4
||
Db 7 NK 8

RESULT 17

Q9R790

ID Q9R790 PRELIMINARY; PRT; 11 AA.
AC Q9R790;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Outer surface protein C (Fragment).
GN OSPC.
OS Borrelia garinii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=29519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G25;
RX MEDLINE=97426044; PubMed=9282748;
RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
RA Rosa P.;
RT "he Borrelia burgdorferi circular plasmid cp26: conservation of
RT plasmid structure and targeted inactivation of the ospC gene.";
RL Mol. Microbiol. 25:361-374(1997).
DR EMBL; U93700; AAC45535.1; -.
DR GO; GO:0009279; C:external outer membrane (sensu Gram-negativ. . .; IEA.
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR InterPro; IPR001800; Lipoprotein_6.
DR Pfam; PF01441; Lipoprotein_6; 1.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1250 MW; 0868D864C5B731A4 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KK 5
||
Db 2 KK 3

RESULT 18

Q47451

ID Q47451 PRELIMINARY; PRT; 11 AA.
AC Q47451;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Plasmid pRJ1004 DNA (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=pRJ1004;
RX MEDLINE=96130847; PubMed=8594334;
RA Brown N.L., Barrett S.R., Camakaris J., Lee B.T., Rouch D.A.;
RT "Molecular genetics and transport analysis of the copper-resistance
RT determinants (pco) from Escherichia coli plasmid pRJ1004.";
RL Mol. Microbiol. 17:1153-1166(1995).
DR EMBL; X83541; CAA58524.1; -.
DR PIR; S70166; S52252.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1195 MW; 47D864F8ADC1A057 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AT 2
||
Db 7 AT 8

RESULT 19
Q9R7U8
ID Q9R7U8 PRELIMINARY; PRT; 11 AA.
AC Q9R7U8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DNR protein (A regulatory protein for the expression of the Nir and
DE nor genes) (Fragment).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PAO1;
RX MEDLINE=95226457; PubMed=7711073;
RA Arai H., Igarashi Y., Kodama T.;
RT "The structural genes for nitric oxide reductase from Pseudomonas
RT aeruginosa.";
RL Biochim. Biophys. Acta 1261:279-284(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PAO1;
RX MEDLINE=95394152; PubMed=7664887;
RA Arai H., Igarashi Y., Kodama T.;
RT "Expression of the nir and nor genes for denitrification of
RT Pseudomonas aeruginosa requires a novel CRP/FNR-related
RT transcriptional regulator, DNR, in addition to ANR.";
RL FEBS Lett. 371:73-76(1995).
DR EMBL; D50019; BAA08746.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1543 MW; DF363CAE141B5736 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 RR 9
||
Db 7 RR 8

RESULT 20
Q9S618
ID Q9S618 PRELIMINARY; PRT; 11 AA.
AC Q9S618;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Cytochrome b6/f complex subunit IV (Fragment).
GN PETD.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanog. 43:1615-1630(1998).
DR EMBL; AF070132; AAD20740.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1297 MW; 5CC38013B7633337 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KK 5
||
Db 5 KK 6

RESULT 21
Q9EUVZ3
ID Q9EUVZ3 PRELIMINARY; PRT; 11 AA.
AC Q9EUVZ3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Ribosome binding factor A (Fragment).
GN RBFA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IQ490;
RA Hedegaard J., Kristensen J.E., Nakamura Y., Sperling-Petersen H.U.,
RA Mortensen K.K.;

RT "Sequence of the infB gene from Escherichia coli strain IQ489 and
RT IQ490.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ132862; CAC20133.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1319 MW; 6B234CFE740879CB CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GR 8
||
Db 6 GR 7

RESULT 22
Q8RMI8
ID Q8RMI8 PRELIMINARY; PRT; 11 AA.
AC Q8RMI8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ErmB (Fragment).
GN ERMB.
OS Enterococcus hirae.
OG Plasmid pMKH1.
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1354;
RN [1]
RP SEQUENCE FROM N.A.
RA Borgen K., Sorum M., Wasteson Y., Kruse H., Oppegaard H.;
RT "Genetic linkage between ermB and vanA in Enterococcus hirae of
RT poultry origin.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF493942; AAM18554.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1359 MW; 08A7A8AA49C7273B CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GR 8
||
Db 9 GR 10

RESULT 23
Q8KTN1
ID Q8KTN1 PRELIMINARY; PRT; 11 AA.
AC Q8KTN1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Phosphoribosylpyrophosphate synthetase (Fragment).
GN PRS.
OS Candidatus Tremblaya princeps.
OC Bacteria; Proteobacteria; Betaproteobacteria; Candidatus Tremblaya.
OX NCBI_TaxID=189385;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22083449; PubMed=12088995;
RA Baumann L., Thao M.L., Hess J.M., Johnson M.W., Baumann P.;
RT "The Genetic Properties of the Primary Endosymbionts of Mealybugs
RT Differ from Those of Other Endosymbionts of Plant Sap-Sucking
RT Insects.";
RL Appl. Environ. Microbiol. 68:3198-3205(2002).
DR EMBL; AF481911; AAM76018.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1127 MW; 4C127758A8676727 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TG 7
||
Db 8 TG 9

RESULT 24
P71228
ID P71228 PRELIMINARY; PRT; 11 AA.
AC P71228;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Nitrate/nitrite sensor transmitter (Fragment).
GN NARQ.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RX MEDLINE=92374842; PubMed=1508040;
RA Chiang R.C., Cavicchioli R., Gunsalus R.P.;
RT "Identification and characterization of narQ, a second nitrate sensor
RT for nitrate-dependent gene regulation in Escherichia coli.";
RL Mol. Microbiol. 6:1913-1923(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RX MEDLINE=97113461; PubMed=8955321;
RA Cavicchioli R., Kolesnikow T., Chiang R.C., Gunsalus R.P.;
RT "Characterization of the aegA locus of Escherichia coli: control of
RT gene expression in response to anaerobiosis and nitrate.";
RL J. Bacteriol. 178:6968-6974(1996).
DR EMBL; L34011; AAB46943.1; -.
FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1200 MW; 52E1CFFCA2D77403 CRC64;
Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RP 10
||
Db 5 RP 6

RESULT 25

Q9K332
ID Q9K332 PRELIMINARY; PRT; 11 AA.
AC Q9K332;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Geh (Fragment).
GN GEH.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS;
RX MEDLINE=20187516; PubMed=10722640;
RA Cramton S.E., Schnell N.F., Gotz F., Bruckner R.;
RT "Identification of a new repetitive element in Staphylococcus
RT aureus.";
RL Infect. Immun. 68:2344-2348(2000).
DR EMBL; AF195967; AAF60251.1; -.
DR EMBL; AF195963; AAF60243.1; -.
DR EMBL; AF195964; AAF60245.1; -.
DR EMBL; AF195965; AAF60247.1; -.
DR EMBL; AF195966; AAF60249.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1262 MW; 4F978F86AAB1A723 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KT 6
||
Db 1 KT 2

RESULT 26

Q9RFZ2
ID Q9RFZ2 PRELIMINARY; PRT; 11 AA.
AC Q9RFZ2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fructose biphosphate aldolase (Fragment).
GN FBA.

OS Mycoplasma mycoides subsp. capri.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=40477;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PG3;
RX MEDLINE=20193983; PubMed=10727835;
RA Thiaucourt F., Lorenzon S., David A., Breard A.;
RT "Phylogeny of the Mycoplasma mycoides cluster as shown by sequencing
RT of a putative membrane protein gene.";
RL Vet. Microbiol. 72:251-268(2000).
DR EMBL; AF162998; AAF15255.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1371 MW; 50B0881A3331FB57 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KK 5
||
Db 7 KK 8

RESULT 27
Q47604
ID Q47604 PRELIMINARY; PRT; 11 AA.
AC Q47604;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE REase protein (Fragment).
GN REASE.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
RT modification systems.";
RL J. Bacteriol. 173:1367-1375(1991).
DR EMBL; M63621; AAA24560.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1296 MW; 3039A71A34472AB7 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NK 4
||
Db 7 NK 8

RESULT 28

Q47345

ID Q47345 PRELIMINARY; PRT; 11 AA.

AC Q47345;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Leader peptide.

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K12;

RA Faber F., van Giezen M., Van Gorcom R.F.M., Harder W.;

RT "Identification of two Escherichia coli K12 proteins which are induced in response to pollutant stress.";

RL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE OF 2-11 FROM N.A.

RC STRAIN=K12;

RX MEDLINE=85134883; PubMed=6396419;

RA Hudson G.S., Davidson B.E.;

RT "Nucleotide sequence and transcription of the phenylalanine and tyrosine operons of Escherichia coli K12.";

RL J. Mol. Biol. 180:1023-1051(1984).

DR EMBL; Z70523; CAA94435.1; -.

SQ SEQUENCE 11 AA; 1402 MW; 87AB199204141775 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 5 PR 6

RESULT 29

Q47420

ID Q47420 PRELIMINARY; PRT; 11 AA.

AC Q47420;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE ORF11 protein.

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K12;

RX MEDLINE=92041688; PubMed=1657895;

RA Sharples G.J., Lloyd R.G.;

RT "Resolution of Holliday junctions in Escherichia coli: Identification

RT of the ruvC gene product as a 19-Kilodalton protein.";
RL J. Bacteriol. 173:7711-7715(1991).
DR EMBL; X59551; CAA42127.1; -.
DR PIR; S19015; S19015.
SQ SEQUENCE 11 AA; 1215 MW; DD8D6D4D56C6D33D CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RP 10
||
Db 2 RP 3

RESULT 30

Q44090
ID Q44090 PRELIMINARY; PRT; 11 AA.
AC Q44090;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical export segment (Fragment).
OS Acholeplasma laidlawii.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Acholeplasma.
OX NCBI_TaxID=2148;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A-EF22;
RA Boyer M.J., Jarhede T.K., Tegman V., Wieslander A.;
RT "Sequence regions from Acholeplasma laidlawii which restore export of
RT beta-lactamase in Escherichia coli.";
RL Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Z22875; CAA80495.1; -.
DR PIR; S33519; S33519.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1234 MW; 5C9D2AE8A682C337 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KK 5
||
Db 2 KK 3

RESULT 31

Q56413
ID Q56413 PRELIMINARY; PRT; 11 AA.
AC Q56413;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IS602L region DNA, 5' end (Fragment).
OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON=Transposon Tn602;
 RX MEDLINE=87318208; PubMed=2819910;
 RA Stibitz S., Davies J.E.;
 RT "Tn602: A naturally occurring relative of Tn903 with direct repeats.";
 RL Plasmid 17:202-209(1987).
 DR EMBL; M22735; AAA27464.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1361 MW; 447E8354A05339C3 CRC64;

 Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 2 TN 3
 ||
 Db 8 TN 9

RESULT 32
 Q47059
 ID Q47059 PRELIMINARY; PRT; 11 AA.
 AC Q47059;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Acetyl ornithine deacetylase (Fragment).
 GN ARGE.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83064529; PubMed=6292860;
 RA Charlier D., Piette J., Glansdorff N.;
 RT "IS3 can function as a mobile promoter in E. coli.";
 RL Nucleic Acids Res. 10:5935-5948(1982).
 DR EMBL; J01589; AAA23485.1; -.
 DR PIR; I41138; I41138.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1181 MW; 93F0429162C05731 CRC64;

 Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 6 TG 7
 ||
 Db 9 TG 10

RESULT 33

Q8GMU3

ID Q8GMU3 PRELIMINARY; PRT; 11 AA.
AC Q8GMU3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative catalase isozyme (Fragment).
GN KATA.
OS Acinetobacter lwoffii.
OG Plasmid pKLH202.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=28090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TC108;
RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
RA Nikiforov V.G.;
RT "pKLH2-like aberrant transposons and possible mechanisms of their
RT dissemination.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ250245; CAC80800.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1233 MW; 81A15757B333276A CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KK 5
||
Db 6 KK 7

RESULT 34

P83537

ID P83537 PRELIMINARY; PRT; 11 AA.
AC P83537;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE, AND INDUCTION.
RC STRAIN=DSM 20451;
RX PubMed=12112860;
RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
RT "High pressure effects step-wise altered protein expression in
RT Lactobacillus sanfranciscensis.";
RL Proteomics 2:765-774(2002).

CC -!- INDUCTION: BY ELEVATED HYDROSTATIC PRESSURE.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN
CC PROTEIN IS: 65 KDA.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1249 MW; D96C8231B771ADD9 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AT 2
||
Db 5 AT 6

RESULT 35
Q9NY38
ID Q9NY38 PRELIMINARY; PRT; 11 AA.
AC Q9NY38;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Heavy metal-responsive transcription factor (Fragment).
GN MTF-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Auf der Maur A., Belser T., Wang Y., Gunes C., Lichtlen P.,
RA Georgiev O., Schaffner W.;
RT "Characterization of the mouse gene for the heavy metal-responsive
RT transcription factor MTF-1.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ251881; CAB71327.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1099 MW; A8653693773772C6 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GR 8
||
Db 8 GR 9

RESULT 36
O60761
ID O60761 PRELIMINARY; PRT; 11 AA.
AC O60761;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE NPT-1 protein (Fragment).
GN NPT-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98207718; PubMed=9545579;
RA Taketani Y., Miyamoto K., Chikamori M., Tanaka K., Yamamoto H.,
RA Tatsumi S., Morita K., Takeda E.;
RT "Characterization of the 5' flanking region of the human NPT-1
RT Na+/phosphate cotransporter gene.";
RL Biochim. Biophys. Acta 1396:267-272(1998).
DR EMBL; D83236; BAA25645.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1358 MW; 884E2D4E6734044A CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KK 5
||
Db 10 KK 11

RESULT 37
Q9H4H5
ID Q9H4H5 PRELIMINARY; PRT; 11 AA.
AC Q9H4H5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE DJ661I20.2 (Novel helicase C-terminal domain and SNF2 N-terminal
DE domains containing protein) (Fragment).
GN DJ620E11.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Skuce C.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL031669; CAC17164.2; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1420 MW; 5EB2C32A3326D053 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KK 5
||
Db 7 KK 8

RESULT 38

Q9UCR1

ID Q9UCR1 PRELIMINARY; PRT; 11 AA.
AC Q9UCR1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AUTOTAXIN (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92129337; PubMed=1733949;
RA Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,
RA Schiffmann E., Liotta L.A.;
RT "Identification, purification, and partial sequence analysis of
RT autotaxin, a novel motility-stimulating protein.";
RL J. Biol. Chem. 267:2524-2529(1992).
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1171 MW; 2723615AA0437737 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AT 2
||
Db 9 AT 10

RESULT 39

Q9UAR8

ID Q9UAR8 PRELIMINARY; PRT; 11 AA.
AC Q9UAR8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sialokinin I preproprotein (Fragment).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rockefeller/Red; TISSUE=Salivary gland;
RX MEDLINE=20099025; PubMed=10620041;
RA Beerntsen B.T., Champagne D.E., Coleman J.L., Campos Y.A., James A.A.;
RT "Characterization of the Sialokinin I gene encoding the salivary
RT vasodilator of the yellow fever mosquito, Aedes aegypti.";
RL Insect Mol. Biol. 8:459-467(1999).
DR EMBL; AF108100; AAD16884.1; -.
DR GO; GO:0007268; P:synaptic transmission; IEA.

DR GO; GO:0007217; P:tachykinin signaling pathway; IEA.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1203 MW; 8BADC77C6B59C33A CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TG 7
||
Db 2 TG 3

RESULT 40

Q9NL65
ID Q9NL65 PRELIMINARY; PRT; 11 AA.
AC Q9NL65;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ASABF-delta (Fragment).
GN ASABF-DELTA.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato Y.;
RT "Ascaris suum asabf-delta gene, exon 2.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB029815; BAA89496.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1187 MW; 8BADD0CD1EAB5861 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TG 7
||
Db 4 TG 5

RESULT 41

P82698
ID P82698 PRELIMINARY; PRT; 11 AA.
AC P82698;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Periviscerokinin-1 (LEM-PVK-1).
OS Leucophaea maderae (Madeira cockroach),
OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),

OS Blaberus craniifer,
 OS Blaptica dubia, and
 OS Gromphadorina portentosa (Cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaeidae.
 OX NCBI_TaxID=6988, 6990, 6982, 132935, 36953;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.
 RC TISSUE=ABDOMINAL PERISYMPATHETIC ORGANS;
 RX MEDLINE=20307624; PubMed=10849006;
 RA Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;
 RT "Identification of novel periviscerokinins from single neurohaemal
 RT release sites in insects. MS/MS fragmentation complemented by Edman
 RT degradation.";
 RL Eur. J. Biochem. 267:3869-3873(2000).
 CC -!- FUNCTION: MEDIATES VISCELAR MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -!- MASS SPECTROMETRY: MW=1090.6; METHOD=MALDI.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
 KW Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1091 MW; 2C2D80E2D7605728 CRC64;

 Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 7 GR 8
 ||
 Db 9 GR 10

RESULT 42
 P82699
 ID P82699 PRELIMINARY; PRT; 11 AA.
 AC P82699;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Periviscerokinin-2 (LEM-PVK-2).
 OS Leucophaeidae maderae (Madeira cockroach),
 OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
 OS Blaberus craniifer,
 OS Blaptica dubia, and
 OS Gromphadorina portentosa (Cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaeidae.
 OX NCBI_TaxID=6988, 6990, 6982, 132935, 36953;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.
 RC TISSUE=ABDOMINAL PERISYMPATHETIC ORGANS;
 RX MEDLINE=20307624; PubMed=10849006;
 RA Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;
 RT "Identification of novel periviscerokinins from single neurohaemal
 RT release sites in insects. MS/MS fragmentation complemented by Edman

RT degradation.";
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -!- FUNCTION: MEDIATES VISCELAR MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -!- MASS SPECTROMETRY: MW=1102.6; METHOD=MALDI.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
KW Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1103 MW; 2F4D9FFD85B05728 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 9 PR 10

RESULT 43

P82700

ID P82700 PRELIMINARY; PRT; 11 AA.
AC P82700;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Periviscerokinin-3 (LEM-PVK-3).
OS Leucophaea maderae (Madeira cockroach),
OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
OS Blaberus craniifer,
OS Blaptica dubia (Argentinian wood cockroach), and
OS Gromphadorina portentosa (Cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988, 6990, 6982, 132935, 36953;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.
RC TISSUE=ABDOMINAL PERISYMPATHETIC ORGANS;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;
RT "Identification of novel periviscerokinins from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation.";
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -!- FUNCTION: MEDIATES VISCELAR MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -!- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
KW Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1147 MW; 2F4D9FF2D7605698 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 9 PR 10

RESULT 44

Q86D32
ID Q86D32 PRELIMINARY; PRT; 11 AA.
AC Q86D32;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Histone H1 (Fragment).
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dm28c;
RX MEDLINE=22557728; PubMed=12670512;
RA Sturm N.R., Vargas N.S., Westenberger S.J., Zingales B.,
RA Campbell D.A.;
RT "Evidence for multiple hybrid groups in Trypanosoma cruzi.";
RL Int. J. Parasitol. 33:269-279(2003).
DR EMBL; AF545075; AAP21903.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1114 MW; CCC1B31E7772CDDD CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KK 5
||
Db 9 KK 10

RESULT 45

Q86D31
ID Q86D31 PRELIMINARY; PRT; 11 AA.
AC Q86D31;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Histone H1 (Fragment).
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sylvio X10;
RX MEDLINE=22557728; PubMed=12670512;
RA Sturm N.R., Vargas N.S., Westenberger S.J., Zingales B.,
RA Campbell D.A.;
RT "Evidence for multiple hybrid groups in Trypanosoma cruzi.";
RL Int. J. Parasitol. 33:269-279(2003).
DR EMBL; AF545076; AAP21906.1; -.

FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1174 MW; CCD1B21E7772CDDD CRC64;
Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KK 5
||
Db 9 KK 10

RESULT 46

Q95PX6

ID Q95PX6 PRELIMINARY; PRT; 11 AA.
AC Q95PX6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN ZK1236.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Favello A.;
RT "The sequence of C. elegans cosmid ZK1236.";
RL Submitted (MAY-1993) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; L13200; AAL11108.1; -.
DR WormPep; ZK1236.8; CE29629.
KW Hypothetical protein.
SQ SEQUENCE 11 AA; 1304 MW; DFA3510A25A76322 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KK 5
||
Db 8 KK 9

RESULT 47

Q9TRW5

ID Q9TRW5 PRELIMINARY; PRT; 11 AA.
AC Q9TRW5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 25 kDa protein P25, peptide F4 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=91372400; PubMed=1909972;
RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,
RA Shiratsuchi A., Uchida T., Imahori K.;
RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a
RT Ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions.";
RL FEBS Lett. 289:37-43(1991).
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1276 MW; CAF72DAF65A76AA9 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GR 8
||
Db 8 GR 9

RESULT 48

Q9TRX0

ID Q9TRX0 PRELIMINARY; PRT; 11 AA.
AC Q9TRX0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Lanosterol 14 alpha-demethylase, cytochrome P-45014DM (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=91316123; PubMed=1859829;
RA Sono H., Sonoda Y., Sato Y.;
RT "Purification and characterization of cytochrome P-45014DM (lanosterol
RT 14 alpha-demethylase) from pig liver microsomes.";
RL Biochim. Biophys. Acta 1078:388-394(1991).
FT NON_TER 1 1
FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1084 MW; 8A7A5CBC2AA72861 CRC64;
Query Match 18.2%; Score 2; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TG 7
||
Db 4 TG 5

RESULT 49
077876
ID 077876 PRELIMINARY; PRT; 11 AA.
AC 077876;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 1 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF049985; AAC41324.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1178 MW; 9AC131FAB2D2DB45 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 TG 7
||
Db 8 TG 9

RESULT 50
Q29831
ID Q29831 PRELIMINARY; PRT; 11 AA.
AC Q29831;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Gene fragment encoding human histocompatibility antigen HLA-DR alpha
DE (exon 2).
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83169718; PubMed=6403940;
RA Das H.K., Biro P.A., Cohen S.N., Erlich H.A., von Gabain A.,
RA Lawrence S.K., Lemaux P.G., McDevitt H.O., Peterlin B.M., Schulz M.F.,
RA Sood A.K., Weissman S.M.;
RT "Use of synthetic oligonucleotide probes complementary to genes for
RT human HLA-DR alpha and beta as extension primers for the isolation of
RT 5' specific clones.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:1531-1535(1983).
DR EMBL; V00525; CAA23784.1; -.
SQ SEQUENCE 11 AA; 1230 MW; 9378714E0865B1EA CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GR 8
||
Db 7 GR 8

RESULT 51
O19718
ID O19718 PRELIMINARY; PRT; 11 AA.
AC O19718;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DRB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86206008; PubMed=3458223;
RA Gregersen P.K., Shen M., Song Q.-L., Merryman P., Degar S., Seki T.,
RA Maccari J., Goldberg D., Murphy H., Schwenzer J., Wang C.Y.,
RA Winchester R.J., Nepom G.T., Silver J.;
RT "Molecular diversity of HLA-DR4 haplotypes.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2642-2646(1986).
DR EMBL; M15074; AAA59810.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1143 MW; 4E6AADA061B776D7 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TG 7
||
Db 7 TG 8

RESULT 52

Q94VG8

ID Q94VG8 PRELIMINARY; PRT; 11 AA.
AC Q94VG8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus gouldii (Gould's monitor).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62042;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407502; AAL10060.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1370 MW; 8E6DEE80C7336411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TN 3
||
Db 10 TN 11

RESULT 53

Q9G5Y6

ID Q9G5Y6 PRELIMINARY; PRT; 11 AA.
AC Q9G5Y6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Agama agama (Red-headed rock agama).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae; Agama.
OX NCBI_TaxID=103336;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128504; AAG00749.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1324 MW; 9D52EC1E336415A1 CRC64;

 Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 5 KT 6
 ||
 Db 3 KT 4

RESULT 54
 Q9G679
 ID Q9G679 PRELIMINARY; PRT; 11 AA.
 AC Q9G679;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Hypsilurus dilophus (Twin-crested anglehead dragon).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
 OC Hypsilurus.
 OX NCBI_TaxID=118208;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128466; AAG00635.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1309 MW; 85F7371E33640451 CRC64;
Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TN 3
||
Db 4 TN 5

RESULT 55

Q94VI5

ID Q94VI5 PRELIMINARY; PRT; 11 AA.
AC Q94VI5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus exanthematicus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=8557;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407496; AAL10043.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1382 MW; 8A26C780C7336411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TN 3
||
Db 10 TN 11

RESULT 56

Q94V74

ID Q94V74 PRELIMINARY; PRT; 11 AA.
AC Q94V74;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Lanthanotus borneensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Lanthanotidae;
OC Lanthanotus.
OX NCBI_TaxID=62058;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407541; AAL10175.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1388 MW; 8F28EE80C7336411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TN 3
||
Db 10 TN 11

RESULT 57
Q9GH12
ID Q9GH12 PRELIMINARY; PRT; 11 AA.
AC Q9GH12;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Photosystem II CP43 apoprotein (Fragment).
GN PSBC.
OS Pandorina morum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Volvocaceae; Pandorina.
OX NCBI_TaxID=33099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UTEX 2326;
RX MEDLINE=20538271; PubMed=11083939;
RA Nozaki H., Misawa K., Kajita T., Kato M., Nohara S., Watanabe M.M.;
RT "Origin and Evolution of the Colonial Volvocales (Chlorophyceae) as
RT Inferred from Multiple, Chloroplast Gene Sequences.";
RL Mol. Phylogenetic Evol. 17:256-268(2000).
DR EMBL; AB044506; BAB18432.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1140 MW; 04E525247731ADDO CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AT 2

||
Db 5 AT 6

RESULT 58
Q94VE7
ID Q94VE7 PRELIMINARY; PRT; 11 AA.
AC Q94VE7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus komodoensis (Komodo dragon).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=61221;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407510; AAL10084.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1370 MW; 8E6DEE80C7336411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TN 3
||
Db 10 TN 11

RESULT 59
Q94VB8
ID Q94VB8 PRELIMINARY; PRT; 11 AA.
AC Q94VB8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus salvatorii (Crocodile monitor).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62049;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).

DR EMBL; AF407522; AAL10119.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1370 MW; 8E6DEE80C7336411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TN 3
||
Db 10 TN 11

RESULT 60
Q94VH7
ID Q94VH7 PRELIMINARY; PRT; 11 AA.
AC Q94VH7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus gilleni (Pygmy mulga monitor).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169840;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407499; AAL10051.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1340 MW; CF6DEE80C733640D CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TN 3
||
Db 10 TN 11

RESULT 61
Q94VK1
ID Q94VK1 PRELIMINARY; PRT; 11 AA.
AC Q94VK1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).

GN COI.
OS Varanus acanthurus (Ridge-tailed monitor).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62035;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407488; AAL10021.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1370 MW; 8E6DEE80C7336411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TN 3
||
Db 10 TN 11

RESULT 62
Q7YKD8
ID Q7YKD8 PRELIMINARY; PRT; 11 AA.
AC Q7YKD8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Photosystem Q(B) protein (Fragment).
GN PSBA.
OS Ribes oxyacanthoides subsp. setosum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;
OC Saxifragales; Grossulariaceae; Ribes.
OX NCBI_TaxID=175229;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulteis L.M., Donoghue M.J.;
RT "Molecular phylogenetic analyses of Ribes (Grossulariaceae) with an
RT emphasis on gooseberries (subg. Grossularia).";
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY138075; AAP92230.1; -.
KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1040 MW; E0210AC9A76DDB0A CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TN 3

||
Db 9 TN 10

RESULT 63
Q7YKC6
ID Q7YKC6 PRELIMINARY; PRT; 11 AA.
AC Q7YKC6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Photosystem Q(B) protein (Fragment).
GN PSBA.
OS Ribes cereum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;
OC Saxifragales; Grossulariaceae; Ribes.
OX NCBI_TaxID=175189;
RN [1]
RP SEQUENCE FROM N.A.
RA Schultheis L.M., Donoghue M.J.;
RT "Molecular phylogenetic analyses of Ribes (Grossulariaceae) with an
RT emphasis on gooseberries (subg. Grossularia).";
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY138087; AAP92242.1; -.
KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1029 MW; D6210AC9A76DDB02 CRC64;
Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TN 3
||
Db 9 TN 10

RESULT 64
Q7YKA6
ID Q7YKA6 PRELIMINARY; PRT; 11 AA.
AC Q7YKA6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Photosystem Q(B) protein (Fragment).
GN PSBA.
OS Itea ilicifolia.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;
OC Saxifragales; Iteaceae; Itea.
OX NCBI_TaxID=96938;
RN [1]
RP SEQUENCE FROM N.A.
RA Schultheis L.M., Donoghue M.J.;

RT "Molecular phylogenetic analyses of Ribes (Grossulariaceae) with an
RT emphasis on gooseberries (subg. Grossularia).";
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY138111; AAP92264.1; -.
KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1029 MW; D6210AC9A76DDB02 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TN 3
||
Db 9 TN 10

RESULT 65
Q7Y9D1
ID Q7Y9D1 PRELIMINARY; PRT; 11 AA.
AC Q7Y9D1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Tympanocryptis houstoni.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
OC Tympanocryptis.
OX NCBI_TaxID=206611;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22653719; PubMed=12769459;
RA Schulte J.A. II, Melville J., Larson A.;
RT "Molecular phylogenetic evidence for ancient divergence of lizard taxa
RT on either side of Wallace's Line.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 270:597-603 (2003).
DR EMBL; AY133028; AAN15907.1; -.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1309 MW; 85F7371E33640451 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TN 3
||
Db 4 TN 5

RESULT 66
Q7Y9B6
ID Q7Y9B6 PRELIMINARY; PRT; 11 AA.
AC Q7Y9B6;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Amphibolurus nobbi.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
OC Amphibolurus.
OX NCBI_TaxID=206551;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22653719; PubMed=12769459;
RA Schulte J.A. II, Melville J., Larson A.;
RT "Molecular phylogenetic evidence for ancient divergence of lizard taxa
on either side of Wallace's Line.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 270:597-603(2003).
DR EMBL; AY132999; AAN15820.1; -.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1309 MW; 85F7371E33640451 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TN 3
||
Db 4 TN 5

RESULT 67
Q38415
ID Q38415 PRELIMINARY; PRT; 11 AA.
AC Q38415;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ant1 protein (Fragment).
OS Bacteriophage P7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC P1-like viruses.
OX NCBI_TaxID=10682;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90335968; PubMed=1696181;
RA Citron M., Schuster H.;
RT "The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.";
RL Cell 62:591-598(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92319637; PubMed=1620606;
RA Citron M., Schuster H.;
RT "The c4 repressor of bacteriophage P1 is a processed 77 base antisense
RNA.";
RL Nucleic Acids Res. 20:3085-3090(1992).

DR EMBL; M35139; AAA32437.1; -.
DR PIR; S42449; S42449.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1315 MW; 38A55C6D11B2C737 CRC64;

Query Match 18.2%; Score 2; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KK 5
||
Db 2 KK 3

RESULT 68

Q37925

ID Q37925 PRELIMINARY; PRT; 11 AA.
AC Q37925;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Bacteriophage fr replicase (Fragment).
OS Bacteriophage fr.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Levivirus.
OX NCBI_TaxID=12017;
RN [1]
RP SEQUENCE FROM N.A.
RA Berzin V.M., Gribanov V.A., Cielens I.E., Jansone I.V., Gren E.J.;
RT "The nucleotide sequence of the regulatory region of phage fr
RT replicase cistron.";
RL Bioorg. Khim. 7:306-308(1981).
DR EMBL; M34834; AAA32193.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1285 MW; 8BD43470C33321B1 CRC64;

Query Match 18.2%; Score 2; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KT 6
||
Db 3 KT 4

RESULT 69

Q06626

ID Q06626 PRELIMINARY; PRT; 11 AA.
AC Q06626;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Patatin A gene protein (Fragment).
GN PATATIN A GENE.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;

OC lamiids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93081729; PubMed=1450383;
RA Nap J.P., Dirkse W.G., Louwerse J., Onstenk J., Visser R., Loonen A.,
RA Heidekamp F., Stiekema W.J.;
RT "Analysis of the region in between two closely linked patatin genes:
RT class II promoter activity in tuber, root and leaf.";
RL Plant Mol. Biol. 20:683-694(1992).
DR EMBL; S51460; AAB24400.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1301 MW; 95577379DB1B1451 CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TN 3
||
Db 4 TN 5

RESULT 70
Q9T0L9
ID Q9T0L9 PRELIMINARY; PRT; 11 AA.
AC Q9T0L9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SLG5 protein (Fragment).
GN SLG5.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99264316; PubMed=10330480;
RA Cabrillac D., Delorme V., Garin J., Ruffio-Chable V., Giranton J.L.,
RA Dumas C., Gaude T., Cock J.M.;
RT "The S15 self-incompatibility haplotype in Brassica includes three S
RT gene family members which are expressed in stigmas.";
RL Plant Cell 11:971-986(1999).
DR EMBL; Y18256; CAB41875.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1035 MW; CD3806DDA8772AAD CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TG 7
||
Db 10 TG 11

RESULT 71

Q8RUE7

ID Q8RUE7 PRELIMINARY; PRT; 11 AA.
AC Q8RUE7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Alcohol dehydrogenase (Fragment).
GN ADH1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Various strains;
RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
RA Morgante M., Rafalski J.A.;
RT "SNP frequency, haplotype structure and linkage disequilibrium in
RT elite maize inbred lines.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF496880; AAM16120.1; -.
DR EMBL; AF496881; AAM16121.1; -.
DR EMBL; AF496882; AAM16122.1; -.
DR EMBL; AF496883; AAM16123.1; -.
DR EMBL; AF496884; AAM16124.1; -.
DR EMBL; AF496885; AAM16125.1; -.
DR EMBL; AF496886; AAM16126.1; -.
DR EMBL; AF496887; AAM16127.1; -.
DR EMBL; AF496888; AAM16128.1; -.
DR EMBL; AF496889; AAM16129.1; -.
DR EMBL; AF496890; AAM16130.1; -.
DR EMBL; AF496891; AAM16131.1; -.
DR EMBL; AF496892; AAM16132.1; -.
DR EMBL; AF496893; AAM16133.1; -.
DR EMBL; AF496894; AAM16134.1; -.
DR EMBL; AF496895; AAM16135.1; -.
DR EMBL; AF496896; AAM16136.1; -.
DR EMBL; AF496897; AAM16137.1; -.
DR EMBL; AF496898; AAM16138.1; -.
DR EMBL; AF496899; AAM16139.1; -.
DR EMBL; AF496900; AAM16140.1; -.
DR EMBL; AF496901; AAM16141.1; -.
DR EMBL; AF496902; AAM16142.1; -.
DR EMBL; AF496903; AAM16143.1; -.
DR EMBL; AF496904; AAM16144.1; -.
DR EMBL; AF496905; AAM16145.1; -.
DR EMBL; AF496906; AAM16146.1; -.
DR EMBL; AF496907; AAM16147.1; -.
DR EMBL; AF496908; AAM16148.1; -.
DR EMBL; AF496909; AAM16149.1; -.
DR EMBL; AF496910; AAM16150.1; -.
DR EMBL; AF496911; AAM16151.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1149 MW; D66AE90942C3387D CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AT 2
||
Db 2 AT 3

RESULT 72

Q04131
ID Q04131 PRELIMINARY; PRT; 11 AA.
AC Q04131;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Wound induced protein (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;
OC lamiids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=pik-red; TISSUE=Pericarp;
RX MEDLINE=91355936; PubMed=1715787;
RA Parsons B.L., Mattoo A.K.;
RT "Wound regulated accumulation of specific transcripts in tomato fruit:
RT interactions with fruit development, ethylene and light.";
RL Plant Mol. Biol. 17:453-464(1991).
DR EMBL; X59884; CAA42539.1; -.
DR PIR; S19775; S19775.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1278 MW; 92CB257828733325 CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KK 5
||
Db 5 KK 6

RESULT 73

P83092
ID P83092 PRELIMINARY; PRT; 11 AA.
AC P83092;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 33.6 kDa protein (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.

OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE, AND SUBCELLULAR LOCATION.
RA Schubert M., Peterson U., Funk C., Schroeder W.P., Kieselbach T.;
RL Submitted (AUG-2001) to Swiss-Prot.
CC --!- SUBCELLULAR LOCATION: CHLOROPLAST; WITHIN THE THYLAKOID LUMEN.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1274 MW; 95344C4D21AAB775 CRC64;
Query Match 18.2%; Score 2; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 10 PR 11

RESULT 74
Q7X9Y3
ID Q7X9Y3 PRELIMINARY; PRT; 11 AA.
AC Q7X9Y3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CUM1 (Fragment).
GN CUM1.
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=3659;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22667639; PubMed=12782724;
RA Hong R.L., Hamaguchi L., Busch M.A., Weigel D.;
RT "Regulatory Elements of the Floral Homeotic Gene AGAMOUS Identified by
RT Phylogenetic Footprinting and Shadowing.";
RL Plant Cell 15:1296-1309(2003).
DR EMBL; AY254704; AAP35238.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1280 MW; D3C7A05641ADD322 CRC64;
Query Match 18.2%; Score 2; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AT 2
||
Db 6 AT 7

RESULT 75
Q99JC3

ID Q99JC3 PRELIMINARY; PRT; 11 AA.
AC Q99JC3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Luteinizing hormone/chorionic gonadotropin receptor homolog
(Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=96147985; PubMed=8571710;
RA Shen Q.X., Liu H.H., Chen W.Y., Bahl O.P.;
RT "[Cloning and overexpression of rat ovary LH/hCG receptor cDNA in
RT insect cells].";
RL Shih Yen Sheng Wu Hsueh Pao 28:283-290(1995).
DR EMBL; S80658; AAB50709.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005213; F:structural constituent of chorion (sensu In. . .; IEA.
KW Chorion; Receptor.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 994 MW; 333DCB137EB865B8 CRC64;

Query Match 18.2%; Score 2; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TG 7
||
Db 3 TG 4

Search completed: April 8, 2004, 15:46:05
Job time : 28.7692 secs

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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 5.15385 Seconds
(without alignments)
111.135 Million cell updates/sec

Title: US-09-787-443A-9

Perfect score: 11

Sequence: 1 ATNKKTGRRPR 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 70

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	3	27.3	11	1	ASL2_BACSE	P83147 bacteroides
2	3	27.3	11	1	TKNA_CHICK	P19850 gallus gall
3	2	18.2	11	1	BPP3_BOTIN	P30423 bothrops in
4	2	18.2	11	1	BPP4_BOTIN	P30424 bothrops in
5	2	18.2	11	1	BPPB_AGKHA	P01021 agkistrodon
6	2	18.2	11	1	BPP_AGKHP	P04562 agkistrodon
7	2	18.2	11	1	BRK_MEGFL	P12797 megascolia
8	2	18.2	11	1	CA21_LITCI	P82087 litoria cit
9	2	18.2	11	1	CA22_LITCI	P82088 litoria cit
10	2	18.2	11	1	CA31_LITCI	P82089 litoria cit
11	2	18.2	11	1	CA32_LITCI	P82090 litoria cit
12	2	18.2	11	1	CA41_LITCI	P82091 litoria cit
13	2	18.2	11	1	CA42_LITCI	P82092 litoria cit
14	2	18.2	11	1	CEP1_ACHFU	P22790 achatina fu
15	2	18.2	11	1	CORZ_PERAM	P11496 periplaneta
16	2	18.2	11	1	FAR6_PENMO	P83321 penaeus mon
17	2	18.2	11	1	OAIF_SARBU	P83518 sarcophaga

18	2	18.2	11	1	PKC1_CARMO	P82684	carausius m
19	2	18.2	11	1	Q2OA_COMTE	P80464	comamonas t
20	2	18.2	11	1	RANC_RANPI	P08951	rana pipien
21	2	18.2	11	1	RR2_CONAM	P42341	conopholis
22	2	18.2	11	1	TIN1_HOPTI	P82651	hoplobatrac
23	2	18.2	11	1	TKN2_UPERU	P08616	uperoleia r
24	2	18.2	11	1	TKNA_GADMO	P28498	gadus morhu
25	2	18.2	11	1	TKNA_HORSE	P01290	equus cabal
26	2	18.2	11	1	TKNA_ONCMY	P28499	oncorhynchus
27	2	18.2	11	1	TKNA_SCYCA	P41333	scyliorhinus
28	2	18.2	11	1	TKN_PHYFU	P08615	physalaemus
29	1	9.1	11	1	ANGT_CRIGE	P09037	crinia georgiana
30	1	9.1	11	1	ASL1_BACSE	P83146	bacteroides
31	1	9.1	11	1	COXA_CANFA	P99501	canis familiaris
32	1	9.1	11	1	CSI5_BACSU	P81095	bacillus subtilis
33	1	9.1	11	1	CX5A_CONAL	P58848	conus aulicus
34	1	9.1	11	1	CX5B_CONAL	P58849	conus aulicus
35	1	9.1	11	1	CXL1_CONMR	P58807	conus marmoreus
36	1	9.1	11	1	EFG_CLOPA	P81350	clostridium
37	1	9.1	11	1	ES1_RAT	P56571	rattus norvegicus
38	1	9.1	11	1	FAR9_CALVO	P41864	calliphora
39	1	9.1	11	1	HS70_PINPS	P81672	pinus pinaster
40	1	9.1	11	1	LADD_ONCMY	P81018	oncorhynchus
41	1	9.1	11	1	LPW_THETH	P05624	thermus thermophilus
42	1	9.1	11	1	LSK1_LEUMA	P04428	leucophaea
43	1	9.1	11	1	LSKP_PERAM	P36885	periplaneta
44	1	9.1	11	1	MHBI_KLEPN	P80580	klebsiella
45	1	9.1	11	1	MLG_THETS	P41989	theromyzon
46	1	9.1	11	1	MORN_HUMAN	P01163	homo sapiens
47	1	9.1	11	1	NUHM_CANFA	P49820	canis familiaris
48	1	9.1	11	1	NXSN_PSETE	P59072	pseudonaja
49	1	9.1	11	1	PQQC_PSEFL	P55173	pseudomonas
50	1	9.1	11	1	PVK1_PERAM	P41837	periplaneta
51	1	9.1	11	1	RE41_LITRU	P82074	litoria rubra
52	1	9.1	11	1	RRPL_CHAV	P13179	chandipura
53	1	9.1	11	1	RS30_ONCMY	P83328	oncorhynchus
54	1	9.1	11	1	T2P1_PROVU	P31031	proteus vulgaris
55	1	9.1	11	1	TIN4_HOPTI	P82654	hoplobatrac
56	1	9.1	11	1	TKC2_CALVO	P41518	calliphora
57	1	9.1	11	1	TKN1_PSEGU	P42986	pseudophryne
58	1	9.1	11	1	TKN1_UPEIN	P82026	uperoleia intermedia
59	1	9.1	11	1	TKN1_UPERU	P08612	uperoleia rufa
60	1	9.1	11	1	TKN2_PSEGU	P42987	pseudophryne
61	1	9.1	11	1	TKN3_PSEGU	P42988	pseudophryne
62	1	9.1	11	1	TKN4_PSEGU	P42989	pseudophryne
63	1	9.1	11	1	TKN5_PSEGU	P42990	pseudophryne
64	1	9.1	11	1	TKNA_RANCA	P22688	rana catesbeiana
65	1	9.1	11	1	TKNA_RANRI	P29207	rana ridibunda
66	1	9.1	11	1	TKND_RANCA	P22691	rana catesbeiana
67	1	9.1	11	1	TKN_ELEMO	P01293	eledone moschata
68	1	9.1	11	1	UF05_MOUSE	P38643	mus musculus
69	1	9.1	11	1	ULAG_HUMAN	P31933	homo sapiens
70	1	9.1	11	1	UXB2 YEAST	P99013	saccharomyces

ALIGNMENTS

RESULT 1

ASL2_BACSE

ID ASL2_BACSE STANDARD; PRT; 11 AA.
 AC P83147;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Acharan sulfate lyase 2 (EC 4.2.2.-) (Fragment).
 OS Bacteroides stercoris.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=46506;
 RN [1]
 RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
 RC STRAIN=HJ-15;
 RX MEDLINE=21223019; PubMed=11322884;
 RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
 RT "Purification and characterization of acharan sulfate lyases, two
 RT novel heparinases, from Bacteroides stercoris HJ-15.";
 RL Eur. J. Biochem. 268:2635-2641(2001).
 CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
 CC heparin and heparan sulfate.
 CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and lead.
 CC Activated by reducing agents, such as DL-dithiothreitol and 2-
 CC mercaptoethanol.
 CC -!- SUBUNIT: Monomer.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
 CC 7.2 and optimum temperature 45 degrees Celsius.
 KW Lyase; Heparin-binding.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1195 MW; D79D897C7AA451AD CRC64;

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATN 3
 |||
 Db 4 ATN 6

RESULT 2

TKNA_CHICK

ID TKNA_CHICK STANDARD; PRT; 11 AA.
 AC P19850;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;

RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=88204263; PubMed=2452461;
 RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
 RT "[Arg3]substance P and neurokinin A from chicken small intestine.";
 RL Regul. Pept. 20:171-180(1988).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 evoke behavioral responses, are potent vasodilators and
 secretagogues, and contract (directly or indirectly) many smooth
 muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; JN0023; JN0023.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

 Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 9 RPR 11
 |||
 Db 1 RPR 3

RESULT 3
 BPP3_BOTIN
 ID BPP3_BOTIN STANDARD; PRT; 11 AA.
 AC P30423;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting
 enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 peptides from Bothrops insularis snake venom.";
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 angiotensin-converting enzyme and enhances the action of
 bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; C37196; C37196.

KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;
Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 5 PR 6

RESULT 4
BPP4_BOTIN
ID BPP4_BOTIN STANDARD; PRT; 11 AA.
AC P30424;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; D37196; D37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1143 MW; 20BBBF13C7741777 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 PR 11
||
Db 5 PR 6

RESULT 5
BPPB_AGKHA
ID BPPB_AGKHA STANDARD; PRT; 11 AA.
AC P01021;

DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide B (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=242054;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Kato H., Suzuki T.;
RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
the venom of Agkistrodon halys blomhoffii.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01254; XASNBA.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 5 PR 6

RESULT 6
BPP_AGKHP
ID BPP_AGKHP STANDARD; PRT; 11 AA.
AC P04562;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys pallas (Chinese water mocassin) (Gloydius halys
OS pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=86177022; PubMed=3008123;
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
RT "Structure-function studies on the bradykinin potentiating peptide
RT from Chinese snake venom (Agkistrodon halys pallas).";

RL Peptides 6 Suppl. 3:339-342(1985).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; JC0002; XAVIBH.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GR 8
||
Db 2 GR 3

RESULT 7
BRK_MEGFL
ID BRK_MEGFL STANDARD; PRT; 11 AA.
AC P12797;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Megascoliakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like
DE peptide ([Thr6]bradykinin)].
OS Megascolia flavifrons (Garden dagger wasp) (Solitary wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Scoliidae; Megascolia.
OX NCBI_TaxID=7437;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=87293024; PubMed=3617088;
RA Yasuhara T., Mantel P., Nakajima T., Piek T.;
RT "Two kinins isolated from an extract of the venom reservoirs of the
RT solitary wasp Megascolia flavifrons.";
RL Toxicon 25:527-535(1987).
RN [2]
RP SEQUENCE.
RC TISSUE=Venom;
RA Nakajima T., Piek T., Yasuhara T., Mantel P.;
RT "Two kinins isolated from the venom of Megascolia flavifrons.";
RL Toxicon 26:34-34(1988).
CC -!- FUNCTION: Both proteins have bradykinin-like, although lower
CC activities (e.g. smooth muscle contraction).
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- SIMILARITY: Belongs to the bradykinin family.
DR PIR; B26744; B26744.
DR GO; GO:0005615; C:extracellular space; IDA.
DR GO; GO:0045776; P:negative regulation of blood pressure; ISS.
DR GO; GO:0045987; P:positive regulation of smooth muscle contra. . .; TAS.
KW Bradykinin; Vasodilator.
FT PEPTIDE 1 11 MEGASCOLIAKININ.

FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.
SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;
Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RP 10
||
Db 1 RP 2

RESULT 8
CA21_LITCI
ID CA21_LITCI STANDARD; PRT; 11 AA.
AC P82087;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 2.1/2.1Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodryadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT montains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 2.1Y4 differs from isoform 2.1 in not being
CC sulfated.
CC -!- MASS SPECTROMETRY: MW=1372; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1312 MW; 10DAB7C4EDD861BB CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 TG 7
||
Db 5 TG 6

RESULT 9

CA22_LITCI

ID CA22_LITCI STANDARD; PRT; 11 AA.
 AC P82088;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 2.2/2.2Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodryadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT montains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 2.2Y4 differs from isoform 2.2 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1328 MW; 10DAB894EDD861BB CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TG 7
 ||
 Db 5 TG 6

RESULT 10

CA31_LITCI

ID CA31_LITCI STANDARD; PRT; 11 AA.
 AC P82089;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 3.1/3.1Y4.

OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodryadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT montains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -!-- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!-- SUBCELLULAR LOCATION: Secreted.
CC -!-- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!-- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being
CC sulfated.
CC -!-- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.
CC -!-- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TG 7
||
Db 6 TG 7

RESULT 11
CA32_LITCI
ID CA32_LITCI STANDARD; PRT; 11 AA.
AC P82090;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 3.2/3.2Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodryadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;

RT "Caerulein-like peptides from the skin glands of the Australian blue mountains tree frog *Litoria citropa*. Part 1. Sequence determination using electrospray mass spectrometry.";
RL *Rapid Commun. Mass Spectrom.* 13:2498-2502(1999).
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 3.2Y4 differs from isoform 3.2 in not being sulfated.
CC -!- MASS SPECTROMETRY: MW=1423; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1363 MW; 10DAB8867861A86B CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TG 7
||
Db 6 TG 7

RESULT 12
CA41_LITCI
ID CA41_LITCI STANDARD; PRT; 11 AA.
AC P82091;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 4.1/4.1Y4.
OS *Litoria citropa* (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodryadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue mountains tree frog *Litoria citropa*. Part 1. Sequence determination using electrospray mass spectrometry.";
RL *Rapid Commun. Mass Spectrom.* 13:2498-2502(1999).
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 4.1Y4 differs from isoform 4.1 in not being sulfated.
CC -!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.

CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1328 MW; 10DAB7C4F5B861BB CRC64;

 Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 6 TG 7
 ||
 Db 5 TG 6

RESULT 13
 CA42_LITCI
 ID CA42_LITCI STANDARD; PRT; 11 AA.
 AC P82092;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 4.2/4.2Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodryadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 4.2Y4 differs from isoform 4.2 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;

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Query Match          18.2%;  Score 2;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.3e+04;
Matches      2;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy          6 TG 7
           ||
Db          5 TG 6

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RESULT 14

CEP1_ACHFU

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ID  CEP1_ACHFU      STANDARD;      PRT;      11 AA.
AC  P22790;
DT  01-AUG-1991 (Rel. 19, Created)
DT  01-AUG-1991 (Rel. 19, Last sequence update)
DT  01-DEC-1992 (Rel. 24, Last annotation update)
DE  Cardio-excitatory peptide-1 (ACEP-1).
OS  Achatina fulica (Giant African snail).
OC  Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC  Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX  NCBI_TaxID=6530;
RN  [1]
RP  SEQUENCE.
RC  STRAIN=Ferussac; TISSUE=Heart atrium;
RX  MEDLINE=90211261; PubMed=2322251;
RA  Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M. ;
RT  "A novel cardio-excitatory peptide isolated from the atria of the
RT  African giant snail, Achatina fulica." ;
RL  Biochem. Biophys. Res. Commun. 167:777-783(1990).
CC  --!- FUNCTION: Potentiates the beat of the ventricle, and has also
CC    excitatory actions on the penis retractor muscle, the buccal
CC    muscle and the identified neurons controlling the buccal muscle
CC    movement of achatina.
CC  --!- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
DR  PIR; A34662; A34662.
KW  Hormone; Amidation.
FT  MOD_RES      11      11      AMIDATION.
SQ  SEQUENCE      11 AA;  1305 MW;  82D6D5B9C7741365 CRC64;

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Query Match          18.2%;  Score 2;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.3e+04;
Matches      2;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy          7 GR 8
           ||
Db          9 GR 10

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RESULT 15

CORZ_PERAM

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ID  CORZ_PERAM      STANDARD;      PRT;      11 AA.
AC  P11496;
DT  01-OCT-1989 (Rel. 12, Created)
DT  01-FEB-1994 (Rel. 28, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Corazonin.
OS  Periplaneta americana (American cockroach).

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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=89325572; PubMed=2753132;
 RA Veenstra J.A.;
 RT "Isolation and structure of corazonin, a cardioactive peptide from
 the American cockroach.";
 RL FEBS Lett. 250:231-234(1989).
 CC -!- FUNCTION: Cardioactive peptide. Corazonin is probably involved
 in the physiological regulation of the heart beat.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR; S05002; S05002.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;

 Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 2 TN 3
 ||
 Db 10 TN 11

RESULT 16
 FAR6_PENMO
 ID FAR6_PENMO STANDARD; PRT; 11 AA.
 AC P83321;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRFamide-like neuropeptide FLP6 (DGRTPALRLRF-amide).
 OS Penaeus monodon (Penoeid shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Penaeus.
 OX NCBI_TaxID=6687;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RX MEDLINE=21956277; PubMed=11959015;
 RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,
 RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
 of the giant tiger prawn Penaeus monodon.";
 RL Comp. Biochem. Physiol. 131B:325-337(2002).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=1301.8; METHOD=MALDI.
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.

KW Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1301 MW; 9A19C860072DC771 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GR 8
||
Db 2 GR 3

RESULT 17
OAI_F_SARBU
ID OAI_F_SARBU STANDARD; PRT; 11 AA.
AC P83518;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ovary-derived ACE interactive factor (Neb-ODAIF) [Contains: Neb-
DE ODAIF(1-9); Neb-ODAIF(1-7)].
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND MASS SPECTROMETRY.
RC TISSUE=Ovary;
RX MEDLINE=22272747; PubMed=12383874;
RA Vandingen A., Hens K., Baggerman G., Macours N., Schoofs L.,
RA De Loof A., Huybrechts R.;
RT "Isolation and characterization of an angiotensin converting enzyme
RT substrate from vitellogenic ovaries of Neobellieria bullata.";
RL Peptides 23:1853-1863(2002).
CC -!- FUNCTION: Substrate for angiotensin converting enzyme (ACE) in
CC vitro.
CC -!- PTM: ACE hydrolyzes Neb-ODAIF by sequentially cleaving off two C-
CC terminal dipeptides.
CC -!- MASS SPECTROMETRY: MW=1312.7; METHOD=MALDI; RANGE=1-11.
CC -!- SIMILARITY: To the N-terminal part of insect vitellogenins.
FT PEPTIDE 1 11 NEB-ODAIF.
FT PEPTIDE 1 9 NEB-ODAIF(1-9).
FT PEPTIDE 1 7 NEB-ODAIF(1-7).
SQ SEQUENCE 11 AA; 1314 MW; 4E114BB566C5A763 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NK 4
||
Db 1 NK 2

RESULT 18

PKC1_CARMO
ID PKC1_CARMO STANDARD; PRT; 11 AA.
AC P82684;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-1 (Cam-PK-1) (FXPRL-Amide).
OS Carausius morosus (Indian stick insect).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatoidea;
OC Heteronemiidae; Carausius.
OX NCBI_TaxID=7022;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RA Predel R., Kellner R., Gaede G.;
RT "Myotropic neuropeptides from the retrocerebral complex of the stick
insect, Carausius morosus (Phasmatodea: Lonchodidae).";
RL Eur. J. Entomol. 96:275-278(1999).
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -!- MASS SPECTROMETRY: MW=1235; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the pyrokinin family.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1236 MW; 2BFA5225BB46C1A8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 PR 11
||
Db 9 PR 10

RESULT 19
Q2OA_COMTE
ID Q2OA_COMTE STANDARD; PRT; 11 AA.
AC P80464;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Quinoline 2-oxidoreductase, alpha chain (EC 1.3.99.17) (Fragment).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Comamonas.
OX NCBI_TaxID=285;
RN [1]
RP SEQUENCE.
RC STRAIN=63;
RX MEDLINE=96035889; PubMed=7556204;
RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;
RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from Comamonas testosteroni 63. The first two enzymes in

RT quinoline and 3-methylquinoline degradation.";
RL Eur. J. Biochem. 232:536-544(1995).
CC -!- FUNCTION: Converts (3-methyl)-quinoline to (3-methyl-)2-oxo-
CC 1,2-dihydroquinoline.
CC -!- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-
CC 1(2H)-one + reduced acceptor.
CC -!- COFACTOR: FAD, molybdenum and iron-sulfur.
CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)quinoline; first
CC step.
CC -!- SUBUNIT: Heterohexamer of two alpha chains, two beta chains, and
CC two gamma chains (Probable).
DR PIR; S66606; S66606.
KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1213 MW; 869094322B1DC2CA CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 10 PR 11

RESULT 20
RANC_RANPI
ID RANC_RANPI STANDARD; PRT; 11 AA.
AC P08951;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranatensin-C.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=84131098; PubMed=6141890;
RA Nakajima T.;
RL Unpublished results, cited by:
RL Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;
RL Comp. Biochem. Physiol. 77C:99-108(1984).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin
CC family.
DR InterPro; IPR000874; Bombesin.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Amphibian defense peptide; Bombesin family; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1304 MW; D6C9885A61ADC366 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AT 2
||
Db 6 AT 7

RESULT 21
RR2_CONAM
ID RR2_CONAM STANDARD; PRT; 11 AA.
AC P42341;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chloroplast 30S ribosomal protein S2 (Fragment).
GN RPS2.
OS Conopholis americana (Squawroot).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;
OC lamiids; Lamiales; Orobanchaceae; Orobancheae; Conopholis.
OX NCBI_TaxID=4179;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92145776; PubMed=1723664;
RA Taylor G., Wolfe K.H., Morden C.W., Depamphilis C.W., Palmer J.D.;
RT "Lack of a functional plastid tRNA(Cys) gene is associated with loss
RT of photosynthesis in a lineage of parasitic plants.";
RL Curr. Genet. 20:515-518(1991).
CC -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X64567; CAA45868.1; -.
DR PIR; S32575; S32575.
DR HAMAP; MF_00291; -; 1.
DR InterPro; IPR001865; Ribosomal_S2.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; PARTIAL.
DR PROSITE; PS00963; RIBOSOMAL_S2_2; PARTIAL.
KW Ribosomal protein; Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1497 MW; 76CD719954536B44 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RR 9
||
Db 3 RR 4

RESULT 22

TIN1_HOPTI

ID TIN1_HOPTI STANDARD; PRT; 11 AA.
 AC P82651;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tigerinin-1.
 OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
 OC Hoplobatrachus.
 OX NCBI_TaxID=103373;
 RN [1]
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
 RC TISSUE=Skin secretion;
 RX PubMed=11031261;
 RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
 RA Devi A.S., Nagaraj R., Sitaram N.;
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
 tigerina.";
 RL J. Biol. Chem. 276:2701-2707(2001).
 CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
 CC S.aureus, M.luteus, P.putida and S.cerevisiae.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- MASS SPECTROMETRY: MW=1342; METHOD=MALDI.
 KW Amphibian defense peptide; Antibiotic; Fungicide; Amidation.
 FT DISULFID 2 10
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
 ||
 Db 8 PR 9

RESULT 23

TKN2_UPERU

ID TKN2_UPERU STANDARD; PRT; 11 AA.
 AC P08616;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Rugosauperolein II ([Lys5,Thr6]physalaemin).
 OS Uperoleia rugosa (Wrinkled toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=8368;
 RN [1]

RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=80223080; PubMed=7389029;
RA Nakajima T., Yasuhara T., Erspamer V., Erspamer G.F., Negri L.;
RT "Physalaemin- and bombesin-like peptides in the skin of the
RT Australian leptodactylid frog *Uperoleia rugosa*.";
RL Chem. Pharm. Bull. 28:689-695(1980).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1270 MW; 3293693E59D1A327 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KT 6
||
Db 5 KT 6

RESULT 24
TKNA_GADMO
ID TKNA_GADMO STANDARD; PRT; 11 AA.
AC P28498;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS *Gadus morhua* (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; *Gadus*.
OX NCBI_TaxID=8049;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92298992; PubMed=1376687;
RA Jensen J., Conlon J.M.;
RT "Substance-P-related and neurokinin-A-related peptides from the brain
RT of the cod and trout.";
RL Eur. J. Biochem. 206:659-664(1992).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.

CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S23306; S23306.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 2 PR 3

RESULT 25
TKNA_HORSE
ID TKNA_HORSE STANDARD; PRT; 11 AA.
AC P01290;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
GN TAC1 OR NKNA OR TAC2 OR NKA.
OS Equus caballus (Horse), and
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796, 10141;
RN [1]
RP SEQUENCE.
RC SPECIES=Horse;
RA Studer R.O., Trzeciak A., Lergier W.;
RT "Isolation and amino-acid sequence of substance P from horse
intestine.";
RL Helv. Chim. Acta 56:860-866(1973).
RN [2]
RP SEQUENCE.
RC SPECIES=C.porcellus;
RX MEDLINE=90044685; PubMed=2478925;
RA Murphy R.;
RT "Primary amino acid sequence of guinea-pig substance P.";
RL Neuropeptides 14:105-110(1989).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; A01558; SPHO.
DR PIR; A60654; A60654.

DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RP 10
||
Db 1 RP 2

RESULT 26

TKNA_ONCMY
ID TKNA_ONCMY STANDARD; PRT; 11 AA.
AC P28499;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92298992; PubMed=1376687;
RA Jensen J., Conlon J.M.;
RT "Substance-P-related and neurokinin-A-related peptides from the brain
RT of the cod and trout.";
RL Eur. J. Biochem. 206:659-664(1992).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S23308; S23308.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 2 PR 3

RESULT 27

TKNA_SCYCA

ID TKNA_SCYCA STANDARD; PRT; 11 AA.
AC P41333;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=93292508; PubMed=7685693;
RA Waugh D., Wang Y., Hazon N., Balment R.J., Conlon J.M.;
RT "Primary structures and biological activities of substance-P-related
RT peptides from the brain of the dogfish, Scyliorhinus canicula.";
RL Eur. J. Biochem. 214:469-474(1993).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S33300; S33300.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D867 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 2 PR 3

RESULT 28

TKN_PHYFU

ID TKN_PHYFU STANDARD; PRT; 11 AA.
AC P08615;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Physalaemin.
OS Physalaemus fuscumaculatus (Neotropical frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;
OC Leptodactylinae; Physalaemus.
OX NCBI_TaxID=8378;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=66076612; PubMed=5857249;
RA Erspamer V., Anastasi A., Bertaccini G., Cei J.M.;
RT "Structure and pharmacological actions of physalaemin, the main
active polypeptide of the skin of Physalaemus fuscumaculatus.";
RL Experientia 20:489-490(1964).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S07201; S07201.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1283 MW; 3293693E59C33457 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NK 4
||
Db 5 NK 6

RESULT 29
ANGT_CRIGE
ID ANGT_CRIGE STANDARD PRT; 11 AA.
AC P09037;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Crinia-angiotensin II.
OS Crinia georgiana (Quacking frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Crinia.
OX NCBI_TaxID=8374;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=80024575; PubMed=488254;

RA Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;
RT "Amino acid composition and sequence of crinia-angiotensin, an
RT angiotensin II-like endecapeptide from the skin of the Australian
RT frog Crinia georgiana.";
RL Experientia 35:1132-1133(1979).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR PIR; S07207; S07207.
KW Vasoconstrictor.
SQ SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 A 1

RESULT 30
ASL1_BACSE
ID ASL1_BACSE STANDARD; PRT; 11 AA.
AC P83146;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acharan sulfate lyase 1 (EC 4.2.2.-) (Fragment).
OS Bacteroides stercoris.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=46506;
RN [1]
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
RC STRAIN=HJ-15;
RX MEDLINE=21223019; PubMed=11322884;
RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
RT "Purification and characterization of acharan sulfate lyases, two
RT novel heparinases, from Bacteroides stercoris HJ-15.";
RL Eur. J. Biochem. 268:2635-2641(2001).
CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
CC heparin and heparan sulfate.
CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and cobalt.
CC Activated by reducing agents, such as DL-dithiothreitol and 2-
CC mercaptoethanol.
CC -!- SUBUNIT: Monomer.
CC -!- PTM: The N-terminus is blocked.
CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
CC 7.2 and optimum temperature 45 degrees Celsius.
KW Lyase; Heparin-binding.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1395 MW; 01B2DAA241E865AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 N 3
|
Db 1 N 1

RESULT 31

COXA_CANFA

ID COXA_CANFA STANDARD; PRT; 11 AA.
AC P99501;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
GN COX5A.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- FUNCTION: This is the heme A-containing chain of cytochrome c
CC oxidase, the terminal oxidase in mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O₂ = 4 ferricytochrome
CC c + 2 H₂O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase Va family.
DR HSC-2DPAGE; P99501; DOG.
DR InterPro; IPR003204; Cyt_c_ox5A.
DR Pfam; PF02284; COX5A; 1.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1274 MW; 910B35C5B1AB11F5 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 T 2
|
Db 7 T 7

RESULT 32

CSI5_BACSU

ID CSI5_BACSU STANDARD; PRT; 11 AA.
AC P81095;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cold shock protein CSI5 (11 kDa cold shock protein) (Fragment).

OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE.
RC STRAIN=168 / JH642;
RA Graumann P.L., Schmid R., Marahiel M.A.;
RL Submitted (OCT-1997) to Swiss-Prot.
RN [2]
RP CHARACTERIZATION.
RC STRAIN=168 / JH642;
RX MEDLINE=96345629; PubMed=8755892;
RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
RT "Cold shock stress-induced proteins in Bacillus subtilis.";
RL J. Bacteriol. 178:4611-4619(1996).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- INDUCTION: In response to low temperature.
CC -!- CAUTION: Could not be found in the genome of B.subtilis 168.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1360 MW; 15F6ECEE6322C330 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 R 8
|
Db 2 R 2

RESULT 33
CX5A_CONAL
ID CX5A_CONAL STANDARD; PRT; 11 AA.
AC P58848;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Conotoxin au5a.
OS Conus aulicus (Court cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89437;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=99452958; PubMed=10521453;
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RT "The T-superfamily of conotoxins.";
RL J. Biol. Chem. 274:30664-30671(1999).
RN [2]
RP ERRATUM.
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;

RL J. Biol. Chem. 274:36030-36030(1999).
 CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is
 CC observed when injected into mice.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1436.6; METHOD=LSIMS.
 CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.
 DR PIR; A59146; A59146.
 KW Toxin.
 FT DISULFID 2 9
 FT DISULFID 3 10
 SQ SEQUENCE 11 AA; 1441 MW; 21A36775440059D7 CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 10 P 10
 |
 Db 4 P 4

RESULT 34
 CX5B_CONAL
 ID CX5B_CONAL STANDARD; PRT; 11 AA.
 AC P58849;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Conotoxin au5b.
 OS Conus aulicus (Court cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=89437;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99452958; PubMed=10521453;
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
 RT "The T-superfamily of conotoxins.";
 RL J. Biol. Chem. 274:30664-30671(1999).
 RN [2]
 RP ERRATUM.
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
 RL J. Biol. Chem. 274:36030-36030(1999).
 CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is
 CC observed when injected into mice (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1388.6; METHOD=LSIMS.
 CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.
 DR PIR; B59146; B59146.

KW Toxin.
FT DISULFID 2 9
FT DISULFID 3 10
SQ SEQUENCE 11 AA; 1393 MW; 21A36775440042D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 P 10
|
Db 4 P 4

RESULT 35
CXL1_CONMR
ID CXL1_CONMR STANDARD PRT; 11 AA.
AC P58807;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lambda-conotoxin CMrVIA.
OS Conus marmoreus (Marble cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=42752;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=20564325; PubMed=10988292;
RA Balaji R.A., Otake A., Sato K., Gopalakrishnakone P., Kini R.M.,
RA Seow K.T., Bay B.-H.;
RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide
RT pattern and protein folding. Isolation and characterization from the
RT venom of Conus marmoreus.";
RL J. Biol. Chem. 275:39516-39522 (2000).
CC -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1237.93; MW_ERR=0.21; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
KW Neurotoxin; Toxin; Hydroxylation.
FT DISULFID 2 11
FT DISULFID 3 8
FT MOD_RES 10 10 HYDROXYLATION.
SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 G 7
|
Db 4 G 4

RESULT 36

EFG_CLOPA

ID EFG_CLOPA STANDARD; PRT; 11 AA.

AC P81350;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Elongation factor G (EF-G) (CP 5) (Fragment).

GN FUSA.

OS Clostridium pasteurianum.

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OC Clostridium.

OX NCBI_TaxID=1501;

RN [1]

RP SEQUENCE.

RC STRAIN=W5;

RX MEDLINE=98291870; PubMed=9629918;

RA Flengsrud R., Skjeldal L.;

RT "Two-dimensional gel electrophoresis separation and N-terminal sequence analysis of proteins from Clostridium pasteurianum W5.";

RL Electrophoresis 19:802-806(1998).

CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of the nascent protein chain from the A-site to the P-site of the ribosome.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family. EF-G/EF-2 subfamily.

DR InterPro; IPR000795; EF_GTPbind.

DR PROSITE; PS00301; EFACTOR_GTP; PARTIAL.

KW Elongation factor; Protein biosynthesis; GTP-binding.

FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 K 4

 |

Db 1 K 1

RESULT 37

ES1_RAT

ID ES1_RAT STANDARD; PRT; 11 AA.

AC P56571;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE ES1 protein, mitochondrial (Fragment).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE.

RC STRAIN=Wistar; TISSUE=Heart;

RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to Swiss-Prot.
CC -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).
CC -!- MISCELLANEOUS: By 2D-PAGE, the determined pI of this protein (spot
CC P2) is: 8.9, its MW is: 25 kDa.
CC -!- SIMILARITY: BELONGS TO THE ES1 FAMILY.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1142 MW; D862272D32C72DC2 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 R 8
|
Db 1 R 1

RESULT 38

FAR9_CALVO
ID FAR9_CALVO STANDARD; PRT; 11 AA.
AC P41864;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 9.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR PIR; I41978; I41978.
KW Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1359 MW; 8160CE46CAA44321 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 N 3
|
Db 3 N 3

RESULT 39

HS70_PINPS

ID HS70_PINPS STANDARD; PRT; 11 AA.
AC P81672;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Heat shock 70 kDa protein (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!-- MISCELLANEOUS: On the 2D-gel the determined pI of this protein
CC (spot N164) is: 5.4, its MW is: 73 kDa.
CC -!-- SIMILARITY: Belongs to the heat shock protein 70 family.
KW ATP-binding; Heat shock; Multigene family.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1228 MW; 037C1BE8DAA44DD0 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 5 A 5

RESULT 40

LADD_ONCMY

ID LADD_ONCMY STANDARD; PRT; 11 AA.
AC P81018;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Ladderlectin (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=97293418; PubMed=9149391;

RA Jensen L.E., Thiel S., Petersen T.E., Jensenuis J.C.;
RT "A rainbow trout lectin with multimeric structure.";
RL Comp. Biochem. Physiol. 116B:385-390(1997).
CC -!- FUNCTION: Lectin that binds sepharose.
CC -!- COFACTOR: Calcium is essential for sepharose binding.
CC -!- SUBUNIT: Multimeric.
KW Lectin; Calcium.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1163 MW; 0B26227FF6D45404 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 A 1

RESULT 41
LPW_THETH
ID LPW_THETH STANDARD; PRT; 11 AA.
AC P05624;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Trp operon leader peptide.
GN TRPL.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermoales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=89000781; PubMed=2844259;
RA Sato S., Nakada Y., Kanaya S., Tanaka T.;
RT "Molecular cloning and nucleotide sequence of Thermus thermophilus
RT HB8 trpE and trpG.";
RL Biochim. Biophys. Acta 950:303-312(1988).
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF TRYPTOPHAN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07744; CAA30565.1; -.
KW Tryptophan biosynthesis; Leader peptide.
SQ SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 A 1
|
Db 2 A 2

RESULT 42
LSK1_LEUMA
ID LSK1_LEUMA STANDARD; PRT; 11 AA.
AC P04428;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Leucosulfakinin-I (LSK-I).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RX MEDLINE=86315858; PubMed=3749893;
RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;
RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to
RT gastrin and cholecystokinin.";
RL Science 234:71-73(1986).
CC --!- FUNCTION: Change the frequency and amplitude of contractions of
CC the hingut. Inhibits muscle contraction of hindgut.
CC --!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A01622; GMROL.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Hormone; Amidation; Sulfation.
FT MOD_RES 6 6 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86B5AAB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 G 7
|
Db 7 G 7

RESULT 43
LSKP_PERAM
ID LSKP_PERAM STANDARD; PRT; 11 AA.
AC P36885;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Perisulfakinin (Pea-SK-I).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90137190; PubMed=2615921;
 RA Veenstra J.A.;
 RT "Isolation and structure of two gastrin/CCK-like neuropeptides from
 RT the American cockroach homologous to the leucosulfakinins.";
 RL Neuropeptides 14:145-149(1989).
 CC -!- FUNCTION: Stimulates hindgut contractions.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR PIR; A60656; A60656.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; 1.
 KW Hormone; Amidation; Sulfation.
 FT MOD_RES 6 6 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAA CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 7 G 7
 |
 Db 7 G 7

RESULT 44
 MHBI_KLEPN
 ID MHBI_KLEPN STANDARD; PRT; 11 AA.
 AC P80580;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Maleylpyruvate isomerase (EC 5.2.1.4) (Fragment).
 GN MHBI.
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96349117; PubMed=8760924;
 RA Robson N.D., Parrott S., Cooper R.A.;
 RT "In vitro formation of a catabolic plasmid carrying Klebsiella
 RT pneumoniae DNA that allows growth of Escherichia coli K-12 on 3-
 RT hydroxybenzoate.";
 RL Microbiology 142:2115-2120(1996).
 CC -!- CATALYTIC ACTIVITY: 3-maleylpyruvate = 3-fumarylpyruvate.
 KW Isomerase.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1387 MW; 1EE0E2DD49C9D5AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 K 4
|
Db 2 K 2

RESULT 45

MLG_THETS

ID MLG_THETS STANDARD; PRT; 11 AA.
AC P41989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin gamma (Gamma-melanocyte stimulating hormone) (Gamma-MSH).
OS Theromyzon tessulatum (Leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
OX NCBI_TaxID=13286;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94298944; PubMed=8026574;
RA Salzet M., Wattez C., Bulet P., Malecha J.;
RT "Isolation and structural characterization of a novel peptide related
RT to gamma-melanocyte stimulating hormone from the brain of the leech
RT Theromyzon tessulatum.";
RL FEBS Lett. 348:102-106(1994).
CC -!- SIMILARITY: Belongs to the POMC family.
DR PIR; S45698; S45698.
KW Hormone; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1486 MW; 2DB8FACE6409C1E8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 K 4
|
Db 10 K 10

RESULT 46

MORN_HUMAN

ID MORN_HUMAN STANDARD; PRT; 11 AA.
AC P01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Morphogenetic neuropeptide (Head activator) (HA).
OS Homo sapiens (Human),
OS Rattus norvegicus (Rat),
OS Bos taurus (Bovine),
OS Anthopleura elegantissima (Sea anemone), and
OS Hydra attenuata (Hydra) (Hydra vulgaris).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
RN [1]
RP SEQUENCE.
RC SPECIES=Human, Rat, and Bovine;
RX MEDLINE=82035850; PubMed=7290191;
RA Bodenmuller H., Schaller H.C.;
RT "Conserved amino acid sequence of a neuropeptide, the head activator,
RT from coelenterates to humans.";
RL Nature 293:579-580(1981).
RN [2]
RP SEQUENCE.
RC SPECIES=A.elegantissima, and H.attenuata;
RA Schaller H.C., Bodenmuller H.;
RT "Isolation and amino acid sequence of a morphogenetic peptide from
RT hydra.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
RN [3]
RP SYNTHESIS.
RX MEDLINE=82050803; PubMed=7297679;
RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;
RT "Synthesis of a new neuropeptide, the head activator from hydra.";
RL FEBS Lett. 131:317-321(1981).
RN [4]
RP FUNCTION.
RX MEDLINE=90059923; PubMed=2583101;
RA Schaller H.C., Druffel-Augustin S., Dubel S.;
RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells
RT in the G2/mitosis transition.";
RL EMBO J. 8:3311-3318(1989).
CC -!- FUNCTION: HA acts as an autocrine growth factor for neural cells
CC in the G2/mitosis transition.
CC -!- CAUTION: This peptide was first isolated from nerve cells of hydra
CC and was called head activator by the authors, because it induced
CC head-specific growth and differentiation in this animal. It has
CC been found in mammalian intestine and hypothalamus.
DR PIR; A01427; YHRT.
DR PIR; A93900; YHXAЕ.
DR PIR; B01427; YHHU.
DR PIR; B93900; YHJFHY.
DR PIR; C01427; YHBO.
DR GK; P01163; -.
KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 G 7
|
Db 4 G 4

RESULT 47

NUHM_CANFA
ID NUHM_CANFA STANDARD; PRT; 11 AA.
AC P49820;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)
DE (EC 1.6.99.3) (Fragment).
GN NDUFV2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
CC TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)
CC FRAGMENT OF THE ENZYME.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC -!- COFACTOR: Binds 1 2Fe-2S cluster (Potential).
CC -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
CC -!- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the
CC mitochondrial inner membrane.
CC -!- SIMILARITY: Belongs to the complex I 24 kDa subunit family.
DR HSC-2DPAGE; P49820; DOG.
DR InterPro; IPR002023; Cmplxl_24kDa.
DR PROSITE; PS01099; COMPLEX1_24K; PARTIAL.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;
KW Iron-sulfur; Iron; 2Fe-2S.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DD8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 G 7
|
Db 1 G 1

RESULT 48
NXSN_PSETE
ID NXSN_PSETE STANDARD; PRT; 11 AA.
AC P59072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Short neurotoxin N1 (Alpha neurotoxin) (Fragment).

OS Pseudonaja textilis (Eastern brown snake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophiinae; Pseudonaja.
 OX NCBI_TaxID=8673;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99449602; PubMed=10518793;
 RA Gong N.L., Armugam A., Jeyaseelan K.;
 RT "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA
 RT cloning, expression and protein characterization.";
 RL Eur. J. Biochem. 265:982-989(1999).
 CC -!- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
 CC acetylcholine receptors (nAChR).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- MASS SPECTROMETRY: MW=6236; METHOD=Electrospray.
 CC -!- MISCELLANEOUS: LD(50) is 0.84 mg/kg by intravenous injection.
 CC -!- SIMILARITY: Belongs to the snake toxin family.
 DR InterPro; IPR003571; Snake_toxin.
 DR PROSITE; PS00272; SNAKE_TOXIN; PARTIAL.
 KW Toxin; Neurotoxin; Postsynaptic neurotoxin;
 KW Acetylcholine receptor inhibitor; Multigene family.
 FT UNSURE 3 3
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1319 MW; 0D1EF0C81B58732B CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 2 T 2
 |
 Db 2 T 2

RESULT 49
 PQQC_PSEFL
 ID PQQC_PSEFL STANDARD; PRT; 11 AA.
 AC P55173;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Coenzyme PQQ synthesis protein C (Pyrroloquinoline quinone
 DE biosynthesis protein C) (Fragment).
 GN PQQC.
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHA0;
 RX MEDLINE=96064397; PubMed=8526497;
 RA Schnider U., Keel C., Defago G., Haas D.;
 RT "Tn5-directed cloning of pqq genes from Pseudomonas fluorescens CHA0:

RT mutational inactivation of the genes results in overproduction of the
RT antibiotic pyoluteorin.";
RL Appl. Environ. Microbiol. 61:3856-3864(1995).
CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
CC -!- SIMILARITY: Belongs to the pqqC family.
CC -----
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CC -----
DR EMBL; X87299; CAA60734.1; -.
DR PIR; S58244; S58244.
DR HAMAP; MF_00654; -; 1.
KW PQQ biosynthesis.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1182 MW; 89DF46E4C5B73771 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 T 2
|
Db 2 T 2

RESULT 50
PVK1_PERAM
ID PVK1_PERAM STANDARD; PRT; 11 AA.
AC P41837;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Periviscerokinin-1 (Pea-PVK-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Abdominal perisynthetic organs;
RX MEDLINE=95232021; PubMed=7716075;
RA Predel R., Linde D., Rapus J., Vettermann S., Penzlin H.;
RT "Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the
RT perisynthetic organs of the American cockroach.";
RL Peptides 16:61-66(1995).
CC -!- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE
CC HYPERNEURAL MUSCLE.
KW Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1114 MW; 39DB5419D7605728 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 G 7
|
Db 1 G 1

RESULT 51

RE41_LITRU

ID RE41_LITRU STANDARD; PRT; 11 AA.
AC P82074;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Rubellidin 4.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodryadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australin red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1039; METHOD=FAB.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1040 MW; 84ED5CBC2877205A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 G 7
|
Db 1 G 1

RESULT 52

RRPL_CHAV

ID RRPL_CHAV STANDARD; PRT; 11 AA.
AC P13179;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)

DE (L protein) (Fragment).
GN L.
OS Chandipura virus (strain I653514).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Vesiculovirus.
OX NCBI_TaxID=11273;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89299473; PubMed=2741347;
RA Masters P.S., Bhella R.S., Butcher M., Patel B., Ghosh H.P.,
RA Banerjee A.K.;
RT "Structure and expression of the glycoprotein gene of Chandipura
RT virus.";
RL Virology 171:285-290(1989).
CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
CC POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS
CC METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).
CC -!- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE
CC NUCLEOCAPSID (N) PROTEIN.
CC -!- SIMILARITY: WITH THE L PROTEIN OF OTHER RHABDOVIRUSES AND
CC PARAMYXOVIRUSES.
CC -----
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CC -----
DR EMBL; J04350; AAA42917.1; -.
KW Transferase; RNA-directed RNA polymerase.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1189 MW; 0335D6E3AAB2D764 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 N 3
|
Db 4 N 4

RESULT 53
RS30_ONCMY
ID RS30_ONCMY STANDARD PRT; 11 AA.
AC P83328;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 40S ribosomal protein S30 (Fragment).
GN FAU.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Skin mucus;
RX MEDLINE=22142142; PubMed=12147245;
RA Fernandes J.M.O., Smith V.J.;
RT "A novel antimicrobial function for a ribosomal peptide from rainbow
RT trout skin.";
RL Biochem. Biophys. Res. Commun. 296:167-171(2002).
CC --!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC --!- MASS SPECTROMETRY: MW=6676.6; METHOD=MALDI.
CC --!- SIMILARITY: Belongs to the S30E family of ribosomal proteins.
KW Ribosomal protein; Antibiotic.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1123 MW; 2312AB630DD735B8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 K 4
|
Db 1 K 1

RESULT 54
T2P1_PROVU
ID T2P1_PROVU STANDARD; PRT; 11 AA.
AC P31031;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Type II restriction enzyme PvuI (EC 3.1.21.4) (Endonuclease PvuI)
DE (R.PvuI) (Fragment).
GN PVUIR.
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
OX NCBI_TaxID=585;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13315;
RX MEDLINE=93087186; PubMed=1454536;
RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
RT "Cloning and characterization of genes for the PvuI restriction and
RT modification system.";
RL Nucleic Acids Res. 20:5743-5747(1992).
CC --!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
CC CLEAVES AFTER T-4.
CC --!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
CC specific double-stranded fragments with terminal 5'-phosphates.
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CC

DR EMBL; L04163; AAA25660.1; -.

DR PIR; S35490; S35490.

DR REBASE; 1541; PvuI.

KW Restriction system; Hydrolase; Nuclease; Endonuclease.

FT NON_TER 1 1

SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 N 3

|

Db 8 N 8

RESULT 55

TIN4_HOPTI

ID TIN4_HOPTI STANDARD PRT; 11 AA.

AC P82654;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Tigerinin-4.

OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;

OC Hoplobatrachus.

OX NCBI_TaxID=103373;

RN [1]

RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.

RC TISSUE=Skin secretion;

RX PubMed=11031261;

RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,

RA Devi A.S., Nagaraj R., Sitaram N.;

RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana tigerina.";

RL J. Biol. Chem. 276:2701-2707(2001).

CC --!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,

CC S.aureus, M.luteus, P.putida and S.cerevisiae.

CC --!- SUBCELLULAR LOCATION: Secreted.

CC --!- TISSUE SPECIFICITY: Skin.

CC --!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.

KW Amphibian defense peptide; Antibiotic.

FT DISULFID 3 11

SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 R 8
|
Db 1 R 1

RESULT 56

TKC2_CALVO
ID TKC2_CALVO STANDARD; PRT; 11 AA.
AC P41518;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Callitachykinin II.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95075727; PubMed=7984492;
RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
RA Naessel D.R.;
RT "Callitachykinin I and II, two novel myotropic peptides isolated from
RT the blowfly, Calliphora vomitoria, that have resemblances to
RT tachykinins.";
RL Peptides 15:761-768(1994).
CC -!- FUNCTION: Myoactive peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1103 MW; 15D7E3F9C9CDD444 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 G 7
|
Db 1 G 1

RESULT 57

TKN1_PSEGU
ID TKN1_PSEGU STANDARD; PRT; 11 AA.
AC P42986;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-I (PG-KI).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]

RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog *Pseudophryne guntheri*.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; B60409; B60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CB1AB7 CRC64;

 Query Match 9.18; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 7 G 7
 |
 Db 9 G 9

RESULT 58
 TKN1_UPEIN
 ID TKN1_UPEIN STANDARD; PRT; 11 AA.
 AC P82026;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Uperin 1.1.
 OS Uperoleia inundata (Floodplain toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=104953;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 RA Adams G.W., Severini C.;
 RT "Novel uperin peptides from the dorsal glands of the australian
 RT floodplain toadlet *Uperoleia inundata*.";
 RL Aust. J. Chem. 49:475-484(1996).

CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=1208; METHOD=FAB.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1226 MW; 3293693E59CDD457 CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 A 1
 |
 Db 2 A 2

RESULT 59
 TKN1_UPERU
 ID TKN1_UPERU STANDARD; PRT; 11 AA.
 AC P08612;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Uperolein.
 OS Uperoleia rugosa (Wrinkled toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=8368;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=75131227; PubMed=1120493;
 RA Anastasi A., Erspermer V., Endean R.;
 RT "Structure of uperolein, a physalaemin-like endecapeptide occurring
 in the skin of Uperoleia rugosa and Uperoleia marmorata.";
 RL Experientia 31:394-395(1975).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 P 10
|
Db 2 P 2

RESULT 60
TKN2_PSEGU
ID TKN2_PSEGU STANDARD; PRT; 11 AA.
AC P42987;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-II (PG-KII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.,
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; C60409; C60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 P 10
|
Db 2 P 2

RESULT 61
TKN3_PSEGU
ID TKN3_PSEGU STANDARD; PRT; 11 AA.
AC P42988;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-III (PG-KIII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; D60409; D60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 N 3
|

Db 5 N 5

RESULT 62
TKN4_PSEGU
ID TKN4_PSEGU STANDARD; PRT; 11 AA.
AC P42989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide I (PG-SPI).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; E60409; E60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 P 10
|
Db 2 P 2

RESULT 63
TKN5_PSEGU
ID TKN5_PSEGU STANDARD; PRT; 11 AA.
AC P42990;

DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide II (PG-SPII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304 (1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; F60409; F60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 P 10
|
Db 2 P 2

RESULT 64
TKNA_RANCA
ID TKNA_RANCA STANDARD; PRT; 11 AA.
AC P22688;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranatachykinin A (RTK A).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain, and Intestine;
 RX MEDLINE=91254337; PubMed=2043143;
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
 RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
 RT brain and intestine.";
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=94023216; PubMed=8210506;
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
 RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
 RT intestine.";
 RL Regul. Pept. 46:81-88(1993).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; A61033; A61033.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1311 MW; 200D60CC59D40AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 K 4
 |
 Db 1 K 1

RESULT 65
 TKNA_RANRI
 ID TKNA_RANRI STANDARD; PRT; 11 AA.
 AC P29207;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranakinin (Substance-P-related peptide).
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;

RX MEDLINE=92044543; PubMed=1658233;
RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
RT neurokinin B from the brain of the frog *Rana ridibunda*.";
RL *J. Neurochem.* 57:2086-2091(1991).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 K 4
|
Db 1 K 1

RESULT 66
TKND_RANCA
ID TKND_RANCA STANDARD; PRT; 11 AA.
AC P22691;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranatachykinin D (RTK D).
OS *Rana catesbeiana* (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Intestine;
RX MEDLINE=91254337; PubMed=2043143;
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation of four novel tachykinins from frog (*Rana catesbeiana*)
RT brain and intestine.";
RL *Biochem. Biophys. Res. Commun.* 177:588-595(1991).
RN [2]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=94023216; PubMed=8210506;
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
RT "Four novel tachykinins in frog (*Rana catesbeiana*) brain and
RT intestine.";
RL *Regul. Pept.* 46:81-88(1993).

CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; D61033; D61033.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; FALSE_NEG.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1350 MW; 3A34256C59D40B07 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 K 4
|
Db 1 K 1

RESULT 67
TKN_ELEMO
ID TKN_ELEMO STANDARD; PRT; 11 AA.
AC P01293;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Eledoisin.
OS Eledone moschata (Musky octopus) (Ozaena moschata), and
OS Eledone cirrhosa (Curled octopus) (Ozaena cirrosa).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Eledone.
OX NCBI_TaxID=6641, 102876;
RN [1]
RP SEQUENCE.
RA Anastasi A., Erspamer V.;
RT "The isolation and amino acid sequence of eledoisin, the active
RT endecapeptide of the posterior salivary glands of Eledone.";
RL Arch. Biochem. Biophys. 101:56-65(1963).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; A01561; EOOC.
DR PIR; B01561; EOOCC.
DR PDB; 1MXQ; 18-FEB-03.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;
KW 3D-structure.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1206 MW; 570D7C2559CDDAA3 CRC64;
Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 P 10
|
Db 2 P 2

RESULT 68
UF05_MOUSE
ID UF05_MOUSE STANDARD PRT; 11 AA.
AC P38643;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P48) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE= Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familiar and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.5, its MW is: 48 kDa.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1328 MW; E54835E5CAAABAFA CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 K 4
|
Db 1 K 1

RESULT 69
ULAG_HUMAN
ID ULAG_HUMAN STANDARD PRT; 11 AA.
AC P31933;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of liver tissue (Spot 118) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94147969; PubMed=8313870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
RT "Human liver protein map: update 1993.";
RL Electrophoresis 14:1216-1222(1993).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.5, its MW is: 34 kDa.
DR SWISS-2DPAGE; P31933; HUMAN.
DR Siena-2DPAGE; P31933; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1219 MW; EDABD37F272DDB0A CRC64;

Query Match 9.18; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 6 A 6

RESULT 70
UXB2_YEAST
ID UXB2_YEAST STANDARD; PRT; 11 AA.
AC P99013;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page (Spot 2D-000K2F) (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RC STRAIN=X2180-1A;
RA Sanchez J.-C., Golaz O., Schaller D., Morch F., Frutiger S.,
RA Hughes G.J., Appel R.D., Deshusses J., Hochstrasser D.F.;
RL Submitted (AUG-1995) to Swiss-Prot.
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.20, its MW is: 9.2 kDa.
DR SWISS-2DPAGE; P99013; YEAST.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1328 MW; EC38021C0DCB42DA CRC64;

Query Match 9.18; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 7 A 7

Search completed: April 8, 2004, 15:47:20
Job time : 5.15385 secs